

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 1, 2005, 08:40:57 ; Search time 18.7599 Seconds
(without alignments)
1690.542 Million cell updates/sec

Title: US-10-624-932-2_COPY_817_898
Perfect score: 432
Sequence: 1 QKIISSLDPPCRRGADWRTL.....AVAGLGQPDAGLFTVSEAE 82

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8						
Result		Query						Description
No.	Score	Match	Length	DB	ID			
1	432	100.0	437	4	AAB50690			Aab50690 Human HS1
2	432	100.0	544	7	ADG42581			Adg42581 Human tra
3	432	100.0	817	8	ADH71624			Adh71624 Human pro
4	432	100.0	833	8	ADH71622			Adh71622 Human pro
5	432	100.0	842	5	AAU74818			Aau74818 Human REP
6	432	100.0	842	8	ADL06574			Adl06574 Human tum
7	432	100.0	898	5	AAU85403			Aau85403 Human pro
8	432	100.0	898	5	AAU97899			Aau97899 Human net
9	432	100.0	898	8	ADH71618			Adh71618 Human pro

10	432	100.0	898	8	ADH71626	Adh71626	Human	pro
11	432	100.0	899	5	AAU79939	Aau79939	Human	UNC
12	432	100.0	899	7	ADG42569	Adg42569	Novel	hum
13	432	100.0	899	8	ADH71636	Adh71636	Human	pro
14	432	100.0	899	8	ADH71642	Adh71642	Human	pro
15	432	100.0	899	8	ADH71648	Adh71648	Human	pro
16	432	100.0	899	8	ADH71632	Adh71632	Human	pro
17	432	100.0	899	8	ADH71610	Adh71610	Human	pro
18	432	100.0	899	8	ADH71628	Adh71628	Human	pro
19	432	100.0	899	8	ADH71640	Adh71640	Human	pro
20	432	100.0	899	8	ADH71630	Adh71630	Human	pro
21	432	100.0	899	8	ADH71644	Adh71644	Human	pro
22	432	100.0	899	8	ADH71634	Adh71634	Human	pro
23	432	100.0	899	8	ADH71646	Adh71646	Human	pro
24	432	100.0	899	8	ADH71638	Adh71638	Human	pro
25	432	100.0	943	4	AAM79128	Aam79128	Human	pro
26	423	97.9	400	7	ADN95115	Adn95115	Human	LEC
27	419	97.0	898	2	AAW78898	Aaw78898	Rat	UNC-5
28	419	97.0	898	5	AAU10543	Aau10543	Rat	netri
29	419	97.0	898	5	AAU97900	Aau97900	Rat	netri
30	419	97.0	898	7	ADG42580	Adg42580	Rat	trans
31	418	96.8	899	8	ADH71650	Adh71650	Human	pro
32	367.5	85.1	436	4	AAM25589	Aam25589	Human	pro
33	363.5	84.1	184	4	AAE09602	Aae09602	Human	gen
34	363.5	84.1	184	4	AAU21749	Aau21749	Novel	hum
35	363.5	84.1	184	5	ABG78974	Abg78974	Human	apo
36	363.5	84.1	184	7	ADC46390	Adc46390	Human	neo
37	363.5	84.1	184	7	AAE39802	Aae39802	Human	gen
38	360	83.3	556	2	AAW78899	Aaw78899	Human	UNC
39	221	51.2	526	4	AAB50648	Aab50648	Human	UNC
40	221	51.2	931	4	AAB50691	Aab50691	Human	UNC
41	221	51.2	931	7	ADE63098	Ade63098	Human	Pro
42	221	51.2	931	7	ADG42584	Adg42584	Human	tra
43	221	51.2	931	7	ABU64297	Abu64297	Human	thr
44	221	51.2	931	8	ADR99258	Adr99258	Human	unc
45	221	51.2	964	8	ADR99250	Adr99250	Human	1RO

ALIGNMENTS

RESULT 1

AAB50690

ID AAB50690 standard; protein; 437 AA.

XX

AC AAB50690;

XX

DT 19-MAR-2001 (first entry)

XX

DE Human HS1 protein SEQ ID NO:89.

XX

KW Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;
KW protein-protein interaction; identification.

XX

OS Homo sapiens.

XX

PN WO200073328-A2.

DE Human transmembrane receptor Unc5H1 homologue.
 XX
 KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
 KW NOVX-associated disorder; cancer; human; transmembrane receptor;
 KW Unc5H1 homologue.
 XX
 OS Homo sapiens.
 XX
 PN US2003204052-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 04-OCT-2001; 2001US-00970944.
 XX
 PR 04-OCT-2000; 2000US-0237862P.
 XX
 PA (HERR/) HERRMANN J L.
 PA (RAST/) RASTELLI L.
 PA (SHIM/) SHIMKETS R A.
 XX
 PI Herrmann JL, Rastelli L, Shimkets RA;
 XX
 DR WPI; 2003-900673/82.
 XX
 PT New NOVX gene or NOVX-specific antibody, useful for preparing a
 PT composition for treating or preventing a NOVX-associated disorder, e.g.,
 PT cancer.
 XX
 PS Disclosure; SEQ ID NO 14; 118pp; English.
 XX
 CC The invention describes a new isolated polypeptide comprising: a
 CC polypeptide or its mature form comprising a sequence not given in the
 CC specification; or a variant of (A), where one or more amino acid residues
 CC in the variant differs in no more than 15% from the amino acid sequence
 CC of the mature form. The pharmaceutical composition may be administered
 CC via oral, transdermal, rectal or parenteral route. The polypeptide,
 CC nucleic acid or antibody is useful for preparing a composition for
 CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
 CC the amino acid sequence of a transmembrane receptor homologue used in a
 CC comparison with the novel human proteins of the invention.
 XX
 SQ Sequence 544 AA;

Query Match 100.0%; Score 432; DB 7; Length 544;
 Best Local Similarity 100.0%; Pred. No. 1.4e-47;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 463 QKIISSLDPPCRRGADWRTLAKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 522
 Qy 61 AA AVAGLGQPDAGLFTVSEAE C 82
 ||||||||||||||||
 Db 523 AA AVAGLGQPDAGLFTVSEAE C 544

ADH71624

ID ADH71624 standard; protein; 817 AA.

XX

AC ADH71624;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21h SEQ ID NO:520.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;

KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

KW obesity; diabetes; infectious disease; metabolic syndrome X;

KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387933P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.

PR 13-JUN-2002; 2002US-0389123P.

PR 14-JUN-2002; 2002US-0389118P.

PR 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389144P.

PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71623.

XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.

PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71621.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 518; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 833 AA;

Query Match 100.0%; Score 432; DB 8; Length 833;

Best Local Similarity 100.0%; Pred. No. 2.5e-47;

Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
|

Db 752 QKIISLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 811

Qy 61 AAVAGLGQPDAGLFTVSEAEC 82

|

Db 812 AAVAGLGQPDAGLFTVSEAEC 833

RESULT 5

AAU74818

ID AAU74818 standard; protein; 842 AA.

XX

AC AAU74818;

XX

DT 23-APR-2002 (first entry)

XX

DE Human REPTR 1 protein.

XX

KW REPTR; human; antiinflammatory; cytostatic; immunosuppressive; antiviral;

KW anti-HIV; antiarthritic; anticonvulsant; nootropic; neuroprotective;

KW antiallergic; antibody; immunogen; endometriosis;

KW gastrointestinal disorder; gastritis; oesophageal carcinoma;

KW Crohn's disease; irritable bowel syndrome; ulcerative colitis;

KW endocrine disorder; hypothalamus disorder; Kallman's disease;

KW autoimmune disease; inflammatory disease; infertility; receptor;

KW acquired immune deficiency syndrome; AIDS; rheumatoid arthritis; allergy;

KW osteoarthritis; diabetes mellitus; multiple sclerosis;

KW systemic lupus erythematosus; cell proliferative disorder; cancer;

KW developmental disorder; Duchenne muscular dystrophy;

KW Becker muscular dystrophy; neurological disorder; epilepsy;

KW Alzheimer's disease; Huntington's disease; reproductive disorder.

XX

OS Homo sapiens.

XX

PN WO200198354-A2.

XX

PD 27-DEC-2001.

XX

PF 21-JUN-2001; 2001WO-US019942.

XX

PR 21-JUN-2000; 2000US-0214027P.

PR 25-AUG-2000; 2000US-0228045P.

PR 12-DEC-2000; 2000US-0255104P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX
PI Griffin JA, Kallick DA, Tribouley CM, Yue H, Nguyen DB, Tang YT;
PI Lal P, Policky JL, Azimzai Y, Lu DAM, Graul R, Yao MG, Burford N;
PI Hafalia AJA, Baughn MR, Bandman O, Patterson C, Yang J, Xu Y;
PI Gandhi AR, Warren BA, Ding L, Sanjanwala MS, Duggan BM, Lu Y;

XX
DR WPI; 2002-090432/12.
DR N-PSDB; ABK15169.

XX
PT Twelve human receptors (referred to as REPTR-1 to REPTR-12), useful in
PT the diagnosis, treatment and prevention of gastrointestinal (e.g.
PT gastritis), autoimmune/inflammatory (e.g. osteoarthritis) and cell
PT proliferative (e.g. cancer) disorders.

XX
PS Claim 45; Page 111-113; 157pp; English.

XX
CC This invention relates to twelve human receptors cDNA sequences referred
CC to as REPTR-1 to REPTR-12), and the proteins encoded thereby. The
CC proteins of the invention may have antiinflammatory, cytostatic,
CC immunosuppressive, antiviral, anti-HIV, antiarthritic, muscular active
CC general, anticonvulsant, nootropic, neuroprotective, antiallergic
CC activities. The sequences of the invention may be used to produce REPTR
CC agonists or antagonists, and the protein sequences may be used to raise
CC anti-REPTR antibodies. These molecules and the REPTR polynucleotides and
CC polypeptides of the invention are useful in the diagnosis, treatment and
CC prevention of gastrointestinal (e.g. gastritis, oesophageal carcinoma,
CC Crohn's disease, irritable bowel syndrome, ulcerative colitis), endocrine
CC (e.g. hypothalamus disorder, Kallman's disease), autoimmune/ inflammatory
CC (e.g. acquired immune deficiency syndrome (AIDS), rheumatoid arthritis,
CC allergies, osteoarthritis, diabetes mellitus, multiple sclerosis,
CC systemic lupus erythematosus), cell proliferative (e.g. cancer),
CC developmental (e.g. Duchenne and Becker muscular dystrophy), neurological
CC (e.g. epilepsy, Alzheimer's disease, Huntington's disease) and
CC reproductive (e.g. infertility, endometriosis) disorders. Numerous other
CC examples of each disorder are given in the specification. The present
CC sequence represents the human REPTR1 protein sequence of the invention

XX
SQ Sequence 842 AA;

Query Match 100.0%; Score 432; DB 5; Length 842;
Best Local Similarity 100.0%; Pred. No. 2.5e-47;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
|
Db 761 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 820

Qy 61 AAAVAGLGQPDAGLFTVSEAE 82
|
Db 821 AAAVAGLGQPDAGLFTVSEAE 842

RESULT 6
ADL06574
ID ADL06574 standard; protein; 842 AA.
XX
AC ADL06574;

XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human tumour-associated antigenic target (TAT) polypeptide #73.
 XX
 KW Human; tumour-associated antigenic target; TAT; cell death; tumour;
 KW cancer; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016225-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 19-AUG-2003; 2003WO-US025892.
 XX
 PR 19-AUG-2002; 2002US-0404809P.
 PR 21-AUG-2002; 2002US-0405645P.
 PR 23-SEP-2002; 2002US-0413192P.
 PR 15-OCT-2002; 2002US-0419008P.
 PR 15-NOV-2002; 2002US-0426847P.
 PR 02-JUL-2003; 2003US-0484959P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
 PI Spencer SD, Wu TD, Zhang Z;
 XX
 DR WPI; 2004-257144/24.
 DR N-PSDB; ADL06497.
 XX
 PT New antibody that binds to a tumor-associated antigenic target (TAT)
 PT polypeptide, useful for preparing a composition for diagnosing or
 PT treating cancer.
 XX
 PS Claim 2; SEQ ID NO 154; 319pp; English.
 XX
 CC The present invention relates to the isolation of human tumour-associated
 CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
 CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
 CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
 CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
 CC produced in bacteria or in CHO cells and induces death of a cell to which
 CC it binds. The antibody is useful for preparing a composition for
 CC diagnosing or treating tumours and cancer. The present sequence
 CC represents a human TAT polypeptide of the invention.
 XX
 SQ Sequence 842 AA;

Query Match 100.0%; Score 432; DB 8; Length 842;
 Best Local Similarity 100.0%; Pred. No. 2.5e-47;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 761 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 820

Qy 61 AAVAGLGQPDAGLFTVSEAEC 82
|||||
Db 821 AAVAGLGQPDAGLFTVSEAEC 842

RESULT 7

AAU85403

ID AAU85403 standard; protein; 898 AA.

XX

AC AAU85403;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human protein NOV1.

XX

KW Human; NOVX; cardiomyopathy; atherosclerosis; diabetes;

KW cell signal processing disorder; metabolic disorder; obesity; infection;

KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;

KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;

KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;

KW psychosis; neurological disorder; anxiety; schizophrenia;

KW manic depression; dementia; dyskinesia; Huntington's disease;

KW Gilles de la Tourette's syndrome; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200210216-A2.

XX

PD 07-FEB-2002.

XX

PF 30-JUL-2001; 2001WO-US024225.

XX

PR 28-JUL-2000; 2000US-0221409P.

PR 04-AUG-2000; 2000US-0222840P.

PR 04-AUG-2000; 2000US-0223752P.

PR 04-AUG-2000; 2000US-0223762P.

PR 04-AUG-2000; 2000US-0223769P.

PR 04-AUG-2000; 2000US-0223770P.

PR 14-AUG-2000; 2000US-0225146P.

PR 15-AUG-2000; 2000US-0225392P.

PR 15-AUG-2000; 2000US-0225470P.

PR 16-AUG-2000; 2000US-0225697P.

PR 01-FEB-2001; 2001US-0263662P.

PR 05-APR-2001; 2001US-0281645P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;

PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;

XX

DR WPI; 2002-180074/23.

DR N-PSDB; ABK37922.

XX

PT New isolated cytoplasmic, nuclear, membrane bound, or secreted

PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,

PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.
XX
PS Claim 1; Page 11; 213pp; English.
XX
CC The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence represents a
CC NOVX protein
XX
SQ Sequence 898 AA;

Query Match 100.0%; Score 432; DB 5; Length 898;
Best Local Similarity 100.0%; Pred. No. 2.7e-47;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
|
Db 817 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 876
Qy 61 AAAVAGLGQPDAGLFTVSEAE 82
|
Db 877 AAAVAGLGQPDAGLFTVSEAE 898

RESULT 8

AAU97899

ID AAU97899 standard; protein; 898 AA.

XX

AC AAU97899;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human netrin binding membrane receptor UNC5H-1 protein.

XX

KW Netrin binding membrane receptor; receptor; UNC5H-1; human; nootropic;
KW neuroprotective; cytostatic; antiparkinsonian; cerebroprotective; cancer;
KW central nervous system; CNS; stroke; Parkinson's disease;

KW multiple sclerosis; Alzheimer's disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 152. .223

FT /note= "Immunoglobulin domain "

FT Domain 247. .294

FT /note= "Thrombospondine type 1 domain "

FT Domain 302. .348

FT /note= "Thrombospondine type 1 domain"

FT Region 361. .382

FT /note= "Transmembrane region"

FT Domain 495. .598

FT /note= "ZU5 domain"

FT Domain 817. .897

FT /note= "Death domain"

XX

PN WO200233080-A2.

XX

PD 25-APR-2002.

XX

PF 15-OCT-2001; 2001WO-EP011891.

XX

PR 16-OCT-2000; 2000US-0240061P.

XX

PA (FARB) BAYER AG.

XX

PI Koehler RH;

XX

DR WPI; 2002-463314/49.

DR N-PSDB; ABK52891.

XX

PT Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.

XX

PS Claim 1; Fig 2; 94pp; English.

XX

CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g, Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents the human netrin binding

CC membrane receptor UNC5H-1 protein of the invention

XX

SQ Sequence 898 AA;

Query Match 100.0%; Score 432; DB 5; Length 898;

Best Local Similarity 100.0%; Pred. No. 2.7e-47;

Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
|||||

Db 817 QKIISLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 876

Qy 61 AA AVAGLGQPDAGLFTVSEAEC 82

|||||

Db 877 AA AVAGLGQPDAGLFTVSEAEC 898

RESULT 9

ADH71618

ID ADH71618 standard; protein; 898 AA.

XX

AC ADH71618;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21e SEQ ID NO:514.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;

KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

KW obesity; diabetes; infectious disease; metabolic syndrome X;

KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.

ADH71626

ID ADH71626 standard; protein; 898 AA.

XX

AC ADH71626;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21i SEQ ID NO:522.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;

KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

KW obesity; diabetes; infectious disease; metabolic syndrome X;

KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387933P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.

PR 13-JUN-2002; 2002US-0389123P.

PR 14-JUN-2002; 2002US-0389118P.

PR 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389144P.

PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71625.

PD 11-APR-2002.
 XX
 PF 04-OCT-2001; 2001WO-US031377.
 XX
 PR 04-OCT-2000; 2000US-0237862P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Herrmann JL, Rastelli L, Shimkets RA;
 XX
 DR WPI; 2002-340104/37.
 DR N-PSDB; ABK49422.
 XX
 PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
 PT treating cardiomyopathy, atherosclerosis, and cancer.
 XX
 PS Claim 1; Page 9; 180pp; English.
 XX
 CC The present invention relates to a new NOVX polypeptide having a 900
 CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
 CC residue amino acid sequence, as given in the specification. The novel
 CC polypeptide, and its encoding polynucleotide, are used to treat
 CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
 CC signal processing and metabolic pathway modulation, in a human. Detecting
 CC the polypeptide or polynucleotide is useful for identifying cancerous
 CC tissue. The antibody can be used to treat diabetes or cancer. The host
 CC cells can be used to produce non-human transgenic animals useful in drug
 CC screening. The present amino acid sequence is that of the human UNC5-like
 CC protein NOV1 of the invention. This sequence is encoded by the human UNC5
 CC -like NOV1 gene located on chromosome 13
 XX
 SQ Sequence 899 AA;

Query Match 100.0%; Score 432; DB 5; Length 899;
 Best Local Similarity 100.0%; Pred. No. 2.7e-47;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 |
 Db 818 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 877
 Qy 61 AAVAGLGQPDAGLFTVSEAEC 82
 |
 Db 878 AAVAGLGQPDAGLFTVSEAEC 899

RESULT 12

ADG42569

ID ADG42569 standard; protein; 899 AA.

XX

AC ADG42569;

XX

DT 26-FEB-2004 (first entry)

XX

DE Novel human NOV1.

XX

KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;

KW NOVX-associated disorder; cancer; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003204052-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 04-OCT-2001; 2001US-00970944.
 XX
 PR 04-OCT-2000; 2000US-0237862P.
 XX
 PA (HERR/) HERRMANN J L.
 PA (RAST/) RASTELLI L.
 PA (SHIM/) SHIMKETS R A.
 XX
 PI Herrmann JL, Rastelli L, Shimkets RA;
 XX
 DR WPI; 2003-900673/82.
 DR N-PSDB; ADG42568.
 XX
 PT New NOVX gene or NOVX-specific antibody, useful for preparing a
 PT composition for treating or preventing a NOVX-associated disorder, e.g.,
 PT cancer.
 XX
 PS Claim 1; SEQ ID NO 2; 118pp; English.
 XX
 CC The invention describes a new isolated polypeptide comprising: a
 CC polypeptide or its mature form comprising a sequence not given in the
 CC specification; or a variant of (A), where one or more amino acid residues
 CC in the variant differs in no more than 15% from the amino acid sequence
 CC of the mature form. The pharmaceutical composition may be administered
 CC via oral, transdermal, rectal or parenteral route. The polypeptide,
 CC nucleic acid or antibody is useful for preparing a composition for
 CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
 CC the amino acid sequence of a human NOVX protein.
 XX
 SQ Sequence 899 AA;

Query Match 100.0%; Score 432; DB 7; Length 899;
 Best Local Similarity 100.0%; Pred. No. 2.7e-47;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 818 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 877

 Qy 61 AAAVAGLGQPDAGLFTVSEAEC 82
 ||||||||||||||||||||
 Db 878 AAAVAGLGQPDAGLFTVSEAEC 899

RESULT 13
 ADH71636
 ID ADH71636 standard; protein; 899 AA.
 XX
 AC ADH71636;

XX
DT 25-MAR-2004 (first entry)
XX
DE Human protein of the invention NOV21n SEQ ID NO:532.
XX
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.

PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
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PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71635.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX
 PS Example 21; SEQ ID NO 532; 1880pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipaemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC represents a NOVX polypeptide of the invention.
 XX
 SQ Sequence 899 AA;

Query Match 100.0%; Score 432; DB 8; Length 899;
 Best Local Similarity 100.0%; Pred. No. 2.7e-47;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 AC ADH71642;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human protein of the invention NOV21q SEQ ID NO:538.
 XX
 KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003102155-A2.
 XX
 PD 11-DEC-2003.
 XX
 PF 03-JUN-2003; 2003WO-US017430.

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PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
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PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
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PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
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PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
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PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
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PR 30-SEP-2002; 2002US-0414839P.
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PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
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PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71641.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 538; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX
SQ Sequence 899 AA;

Query Match 100.0%; Score 432; DB 8; Length 899;
Best Local Similarity 100.0%; Pred. No. 2.7e-47;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 AAAVAGLGQPDAGLFTVSEAEC 82
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RESULT 15

ADH71648

ID ADH71648 standard; protein; 899 AA.

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AC ADH71648;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV21t SEQ ID NO:544.

XX

KW human; cytostatic; immunomodulator; neuroprotective; nootropic;

KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

KW obesity; diabetes; infectious disease; metabolic syndrome X;

KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

PF 03-JUN-2003; 2003WO-US017430.

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PR 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

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PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
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PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
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PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
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PR 26-AUG-2002; 2002US-0406355P.
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PR 05-NOV-2002; 2002US-00423798.

PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX

PA (CURA-) CURAGEN CORP.

XX

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PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
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PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX

DR WPI; 2004-081935/08.

DR N-PSDB; ADH71647.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX

PS Example 21; SEQ ID NO 544; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 899 AA;

Query Match 100.0%; Score 432; DB 8; Length 899;

Best Local Similarity 100.0%; Pred. No. 2.7e-47;

Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
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Db 818 QKIISSLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 877

Qy 61 AAVAGLGQPDAGLFTVSEAE C 82
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GenCore version 5.1.6
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SUMMARIES

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3	360.5	83.4	557	2	US-08-808-982-6	Sequence 6, Appli
4	360.5	83.4	557	3	US-09-306-902A-6	Sequence 6, Appli
5	221	51.2	769	4	US-09-949-016-10665	Sequence 10665, A
6	205	47.5	943	2	US-08-808-982-7	Sequence 7, Appli
7	205	47.5	943	3	US-09-306-902A-7	Sequence 7, Appli
8	190	44.0	655	4	US-09-969-532-32	Sequence 32, Appl
9	190	44.0	666	4	US-09-969-532-30	Sequence 30, Appl
10	190	44.0	669	4	US-09-969-532-28	Sequence 28, Appl
11	190	44.0	680	4	US-09-969-532-26	Sequence 26, Appl

12	190	44.0	886	4	US-09-969-532-16	Sequence 16, Appl
13	190	44.0	897	4	US-09-969-532-14	Sequence 14, Appl
14	190	44.0	900	4	US-09-969-532-12	Sequence 12, Appl
15	190	44.0	911	4	US-09-969-532-10	Sequence 10, Appl
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38	63.5	14.7	493	3	US-09-136-828-2	Sequence 2, Appli
39	63.5	14.7	493	3	US-09-332-928A-2	Sequence 2, Appli
40	63.5	14.7	493	4	US-09-136-801-2	Sequence 2, Appli
41	63.5	14.7	493	4	US-09-332-929-2	Sequence 2, Appli
42	63.5	14.7	493	4	US-09-333-075-2	Sequence 2, Appli
43	63.5	14.7	493	4	US-09-202-088A-2	Sequence 2, Appli
44	63.5	14.7	493	4	US-09-333-077-2	Sequence 2, Appli
45	63.5	14.7	493	4	US-10-018-386-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-808-982-5

; Sequence 5, Application US/08808982

; Patent No. 5939271

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; APPLICANT: Leonardo, E. David

; APPLICANT: Hink, Lindsay

; APPLICANT: Masu, Masayuki

; APPLICANT: Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA


```

;           ZIP: 94104
;
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/306,902A
;       FILING DATE: 07-May-1999
;       CLASSIFICATION: <Unknown>
;
;   ATTORNEY/AGENT INFORMATION:
;       NAME: OSMAN, RICHARD A
;       REGISTRATION NUMBER: 36,627
;       REFERENCE/DOCKET NUMBER: UC96-217
;
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (415) 343-4341
;       TELEFAX: (415) 343-4342
;
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 898 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: not relevant
;           TOPOLOGY: not relevant
;
;       MOLECULE TYPE: peptide
;
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-306-902A-5

```

```

Query Match          97.0%;  Score 419;  DB 3;  Length 898;
Best Local Similarity 96.3%;  Pred. No. 1.6e-47;
Matches 79;  Conservative 1;  Mismatches 2;  Indels 0;  Gaps 0;

```

```

Qy      1 QKIISLDPPCRGRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
        ||||:||||| |||||||||||||||||||||||||||||||||||||||||
Db      817 QKIIASLDPPCSRGRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLGQL 876

Qy      61 AAVAGLGQPDAGLFTVSEAEC 82
        ||||||||||||||||||
Db      877 AAVAGLGQPDAGLFTVSEAEC 898

```

RESULT 3

US-08-808-982-6

```

; Sequence 6, Application US/08808982
; Patent No. 5939271
;   GENERAL INFORMATION:
;       APPLICANT: Tessier-Lavigne, Marc
;       APPLICANT: Leonardo, E. David
;       APPLICANT: Hink, Lindsay
;       APPLICANT: Masu, Masayuki
;       APPLICANT: Kazuko, Keino-Masu
;       TITLE OF INVENTION: Netrin Receptors
;       NUMBER OF SEQUENCES: 8
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;           STREET: 268 BUSH STREET, SUITE 3200
;           CITY: SAN FRANCISCO
;           STATE: CALIFORNIA

```

```

; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-808-982-6

```

```

Query Match          83.4%; Score 360.5; DB 2; Length 557;
Best Local Similarity 86.7%; Pred. No. 6.6e-40;
Matches 72; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

```

```

Qy      1 QKIISSLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      475 QKIISSLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 534

Qy      61 AAVAGLGQPDAGLFT-VSEAEC 82
        ||||| | : |||||
Db      535 AAVAGTXPAGRWLLSQCEAEC 557

```

RESULT 4

US-09-306-902A-6

; Sequence 6, Application US/09306902A

; Patent No. 6277585

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

```

;          COUNTRY: USA
;          ZIP: 94104
;    COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/306,902A
;          FILING DATE: 07-May-1999
;          CLASSIFICATION: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;          NAME: OSMAN, RICHARD A
;          REGISTRATION NUMBER: 36,627
;          REFERENCE/DOCKET NUMBER: UC96-217
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (415) 343-4341
;          TELEFAX: (415) 343-4342
;    INFORMATION FOR SEQ ID NO: 6:
;          SEQUENCE CHARACTERISTICS:
;            LENGTH: 557 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: not relevant
;            TOPOLOGY: not relevant
;          MOLECULE TYPE: peptide
;          SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-306-902A-6

```

```

Query Match          83.4%;  Score 360.5;  DB 3;  Length 557;
Best Local Similarity 86.7%;  Pred. No. 6.6e-40;
Matches 72;  Conservative 1;  Mismatches 9;  Indels 1;  Gaps 1;

```

```

Qy      1 QKIISSLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      475 QKIISSLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 534

Qy      61 AAVAGLGQPDAGLFT-VSEAEC 82
        |||||  | : |||||
Db      535 AAVAGTXPAGRWLLSQCSEAEC 557

```

RESULT 5

```

US-09-949-016-10665
; Sequence 10665, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

```

; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10665
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10665

Query Match 51.2%; Score 221; DB 4; Length 769;
Best Local Similarity 51.9%; Pred. No. 7.2e-21;
Matches 42; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
||: |||| | || ||| || ||: || :||: ||: || || :||: ||||: ||: |||| |
Db 688 QKLCSSLDAPQTRGHDWRMLAHKLNLDRLNYFATKSSPTGVILDLWEAQNFDPGNLSML 747

Qy 61 AAVAGLGQPDAGLFTVSEAE 81
|| : ||: : : : | :
Db 748 AAVLEEMGRHETVVSIAEGQ 768

RESULT 6

US-08-808-982-7

; Sequence 7, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-808-982-7

Query Match 47.5%; Score 205; DB 2; Length 943;
Best Local Similarity 47.6%; Pred. No. 1.4e-18;
Matches 39; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLDHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
||| :||| | || ||| |||| :| :||:|:| ||| :||:|||| :||:|
Db 862 QKICNSLDAPNSRGNDWRLLAQKLSDRYLNYPATKASPTGVILDLEWARQQDDGDLNSL 921

Qy 61 AAVAGLGQPDAGLFTVSEAE 82
|:|: |:|: : : : : :
Db 922 ASALEEMGKSEMLVAMTTDGDC 943

RESULT 7

US-09-306-902A-7

; Sequence 7, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-306-902A-7

Query Match 47.5%; Score 205; DB 3; Length 943;
Best Local Similarity 47.6%; Pred. No. 1.4e-18;
Matches 39; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
||| :||| | || ||| |||| :| :||:|:| ||| :||:|||| :|:|: |
Db 862 QKICNSLDAPNSRGNDWRLLAQKLSDRYLNyFATKASPTGVILDLWEARQQDDGDLNSL 921

Qy 61 AAVAGLGQPDAGLFTVSEAE 82
|:|: |:|: : : : : : :
Db 922 ASALEEMGKSEMLVAMTTDGDC 943

RESULT 8

US-09-969-532-32
; Sequence 32, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 655
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-32

Query Match 44.0%; Score 190; DB 4; Length 655;
Best Local Similarity 44.4%; Pred. No. 8.9e-17;
Matches 36; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
|:| :|: | | :| ||: |||| :| :||:|:|: ||:|:||||||| :|:| |
Db 561 QRICATFDTPNAGKGDWQMLAQKNSINRNLSyFATQSSPSAVILNLWEARHQHDGDLDSL 620

Qy 61 AAVAGLGQPDAGLFTVSEAE 81
| |: |:|: | :||:|:
Db 621 ACALEEIGRTHTKLSNISESQ 641

RESULT 9

US-09-969-532-30

; Sequence 30, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 666

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-969-532-30

Query Match 44.0%; Score 190; DB 4; Length 666;

Best Local Similarity 44.4%; Pred. No. 9.1e-17;

Matches 36; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60

|:| :: | | :| ||: |||| :: :||:|:: ||:|:||||||| |:| |

Db 572 QRICATFDTPNAKGKDWQMLAQKNSINRNLSYFATQSSPSAVILNLWEARHQHDGDLDSL 631

Qy 61 AAVAGLGQPDAGLFTVSEAE 81

| |: |: | :||:

Db 632 ACALEEIGRTHTKLSNISESQ 652

RESULT 10

US-09-969-532-28

; Sequence 28, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 669

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-969-532-28

Query Match 44.0%; Score 190; DB 4; Length 669;
Best Local Similarity 44.4%; Pred. No. 9.2e-17;
Matches 36; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
|:| :: | | :| ||: ||| :: :||:|:: ||:|:||||||| |:| |
Db 575 QRICATFDT PNAKGKDWQMLAQKNSINRNLSYFATQSSPSAVILNLWEARHQHDGDLDSL 634

Qy 61 AA AVAGLGQPDAGLFTVSEAE 81
| |: |: | :||:
Db 635 ACALEEIGRTHTKLSNISESQ 655

RESULT 11

US-09-969-532-26

; Sequence 26, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 680
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-26

Query Match 44.0%; Score 190; DB 4; Length 680;
Best Local Similarity 44.4%; Pred. No. 9.4e-17;
Matches 36; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
|:| :: | | :| ||: ||| :: :||:|:: ||:|:||||||| |:| |
Db 586 QRICATFDT PNAKGKDWQMLAQKNSINRNLSYFATQSSPSAVILNLWEARHQHDGDLDSL 645

Qy 61 AA AVAGLGQPDAGLFTVSEAE 81
| |: |: | :||:
Db 646 ACALEEIGRTHTKLSNISESQ 666

RESULT 12

US-09-969-532-16

; Sequence 16, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John

```
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 886
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-16
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```
Query Match          44.0%; Score 190; DB 4; Length 886;
Best Local Similarity 44.4%; Pred. No. 1.3e-16;
Matches 36; Conservative 21; Mismatches 24; Indels 0; Gaps 0;
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```
Qy      1 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
      |:| :: | | :| ||: |||| :: :||:|::: ||:|:||||||| |:| |
Db      792 QRICATFDTNPAKGKDWQMLAQKNSINRNLSYFATQSSPSAVILNLWEARHQHGDGLDSL 851

Qy      61 AAVAGLGQPDAGLFTVSEAE 81
      | |: |: | :||:
Db      852 ACALEEIGRTHTKLSNISESQ 872
```

RESULT 13

```
US-09-969-532-14
; Sequence 14, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
Encoding the Same
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 897
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-14
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Query Match          44.0%; Score 190; DB 4; Length 897;
Best Local Similarity 44.4%; Pred. No. 1.4e-16;
Matches 36; Conservative 21; Mismatches 24; Indels 0; Gaps 0;
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```
Qy      1 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
      |:| :: | | :| ||: |||| :: :||:|::: ||:|:||||||| |:| |
Db      803 QRICATFDTNPAKGKDWQMLAQKNSINRNLSYFATQSSPSAVILNLWEARHQHGDGLDSL 862
```

Qy 61 AAVAVAGLGQPDAGLFTVSEAE 81
 | |: |: | :|::
 Db 863 ACALEEIGRTHTKLSNISESQ 883

RESULT 14

US-09-969-532-12

; Sequence 12, Application US/09969532
 ; Patent No. 6777232
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Scoville, John
 ; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
 Encoding the Same
 ; FILE REFERENCE: LEX-0244-USA
 ; CURRENT APPLICATION NUMBER: US/09/969,532
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US 60/237,280
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 900
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-09-969-532-12

Query Match 44.0%; Score 190; DB 4; Length 900;
 Best Local Similarity 44.4%; Pred. No. 1.4e-16;
 Matches 36; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 |:| :: | | :| ||: ||| :: :||:|:: ||:|:||||||| :|:| |
 Db 806 QRICATFDTPNAKGKDWQMLAQKNSINRNLSYFATQSSPSAVILNLWEARHQHGDGLDSL 865

 Qy 61 AAVAVAGLGQPDAGLFTVSEAE 81
 | |: |: | :|::
 Db 866 ACALEEIGRTHTKLSNISESQ 886

RESULT 15

US-09-969-532-10

; Sequence 10, Application US/09969532
 ; Patent No. 6777232
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Scoville, John
 ; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides
 Encoding the Same
 ; FILE REFERENCE: LEX-0244-USA
 ; CURRENT APPLICATION NUMBER: US/09/969,532
 ; CURRENT FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US 60/237,280
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 10
; LENGTH: 911
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-969-532-10

Query Match 44.0%; Score 190; DB 4; Length 911;
Best Local Similarity 44.4%; Pred. No. 1.4e-16;
Matches 36; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLDHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
|:| :: | | :| ||: ||| :: :||:|:: ||:|:||||| |:| |
Db 817 QRICATFDTPNAKGKDWQMLAQKNSINRNLSYFATQSSPSAVILNLWEARHQHDGDLDSL 876

Qy 61 AAVAGLGQPDAGLFTVSEAE 81
| |: |: | :||:
Db 877 ACALEEIGRTHTKLSNISESQ 897

Search completed: March 1, 2005, 09:05:54
Job time : 5.9133 secs

OM protein - protein search, using sw model

Run on: March 1, 2005, 09:06:01 ; Search time 15.7821 Seconds
(without alignments)
1704.439 Million cell updates/sec

Title: US-10-624-932-2_COPY_817_898
Perfect score: 432
Sequence: 1 QKIISSLDPPCRRGADWRTL.....AVAGLGQPDAGLFTVSEAE 82

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	432	100.0	544	10	US-09-970-944-14	Sequence 14, Appl
2	432	100.0	842	15	US-10-311-623-1	Sequence 1, Appli
3	432	100.0	898	10	US-09-918-779-2	Sequence 2, Appli
4	432	100.0	898	15	US-10-624-932-2	Sequence 2, Appli
5	432	100.0	899	10	US-09-970-944-2	Sequence 2, Appli
6	419	97.0	898	10	US-09-933-261-5	Sequence 5, Appli
7	419	97.0	898	10	US-09-970-944-13	Sequence 13, Appl
8	419	97.0	898	14	US-10-256-702-5	Sequence 5, Appli
9	419	97.0	898	14	US-10-240-154-16	Sequence 16, Appl
10	367.5	85.1	436	15	US-10-296-115-1104	Sequence 1104, Ap
11	363.5	84.1	184	9	US-09-764-861-38	Sequence 38, Appl
12	363.5	84.1	184	10	US-09-764-861-38	Sequence 38, Appl
13	363.5	84.1	184	14	US-10-103-313-476	Sequence 476, App
14	363.5	84.1	184	14	US-10-115-928-38	Sequence 38, Appl
15	360.5	83.4	557	10	US-09-933-261-6	Sequence 6, Appli
16	360.5	83.4	557	14	US-10-256-702-6	Sequence 6, Appli
17	221	51.2	931	10	US-09-970-944-15	Sequence 15, Appl
18	221	51.2	931	10	US-09-970-944-16	Sequence 16, Appl
19	221	51.2	931	10	US-09-970-944-17	Sequence 17, Appl
20	221	51.2	931	11	US-09-972-211-121	Sequence 121, App
21	221	51.2	931	11	US-09-972-211-122	Sequence 122, App
22	221	51.2	931	11	US-09-972-211-125	Sequence 125, App
23	221	51.2	931	15	US-10-087-684-35	Sequence 35, Appl
24	221	51.2	931	15	US-10-087-684-36	Sequence 36, Appl
25	221	51.2	931	15	US-10-218-779-36	Sequence 36, Appl
26	221	51.2	931	15	US-10-037-417-117	Sequence 117, App
27	221	51.2	931	15	US-10-037-417-118	Sequence 118, App
28	221	51.2	931	15	US-10-037-417-119	Sequence 119, App
29	221	51.2	931	15	US-10-037-417-120	Sequence 120, App
30	221	51.2	931	15	US-10-096-625-121	Sequence 121, App
31	221	51.2	931	15	US-10-096-625-122	Sequence 122, App
32	221	51.2	931	15	US-10-096-625-125	Sequence 125, App
33	221	51.2	1010	15	US-10-218-779-35	Sequence 35, Appl
34	208	48.1	945	11	US-09-972-211-123	Sequence 123, App
35	208	48.1	945	15	US-10-087-684-33	Sequence 33, Appl
36	208	48.1	945	15	US-10-218-779-33	Sequence 33, Appl
37	208	48.1	945	15	US-10-096-625-123	Sequence 123, App
38	205	47.5	943	10	US-09-933-261-7	Sequence 7, Appli
39	205	47.5	943	14	US-10-256-702-7	Sequence 7, Appli
40	205	47.5	945	11	US-09-972-211-124	Sequence 124, App
41	205	47.5	945	15	US-10-087-684-34	Sequence 34, Appl
42	205	47.5	945	15	US-10-218-779-34	Sequence 34, Appl
43	205	47.5	945	15	US-10-037-417-121	Sequence 121, App
44	205	47.5	945	15	US-10-096-625-124	Sequence 124, App
45	199	46.1	554	15	US-10-108-260A-2682	Sequence 2682, Ap

ALIGNMENTS

RESULT 1

US-09-970-944-14

; Sequence 14, Application US/09970944

; Publication No. US20030204052A1

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; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1 Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-944-14
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Best Local Similarity 100.0%; Pred. No. 1.7e-46;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

US-10-311-623-1

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; Sequence 1, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
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; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CD1
US-10-311-623-1
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Best Local Similarity 100.0%; Pred. No. 2.9e-46;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3

US-09-918-779-2

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; Sequence 2, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
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; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-779-2
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Query Match          100.0%; Score 432; DB 10; Length 898;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4

US-10-624-932-2

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; Sequence 2, Application US/10624932
; Publication No. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
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; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-624-932-2

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Query Match          100.0%; Score 432; DB 15; Length 898;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
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Db      817 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 876

Qy      61 AAVAGLGQPDAGLFTVSEAE C 82
        ||||||||||||||||
Db      877 AAVAGLGQPDAGLFTVSEAE C 898

```

RESULT 5

US-09-970-944-2

; Sequence 2, Application US/09970944

; Publication No. US20030204052A1

; GENERAL INFORMATION:

; APPLICANT: Herrman, John L

; APPLICANT: Rastelli, Luca

; APPLICANT: Shimkets, Richard A

; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same and

; TITLE OF INVENTION: Antibodies Directed Against these Proteins

; FILE REFERENCE: 21402-138

; CURRENT APPLICATION NUMBER: US/09/970,944

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 60/237,862

; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 899

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-970-944-2

Query Match 100.0%; Score 432; DB 10; Length 899;

Best Local Similarity 100.0%; Pred. No. 3.1e-46;

Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60

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Qy 61 AAVAGLGQPDAGLFTVSEAE C 82

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Db 878 AAVAGLGQPDAGLFTVSEAE C 899

RESULT 6

US-09-933-261-5

; Sequence 5, Application US/09933261

; Publication No. US20030040046A1

; GENERAL INFORMATION:

; APPLICANT: Tessier-Lavigne, Marc

; Leonardo, E. David

; Hink, Lindsay

; Masu, Masayuki

; Kazuko, Keino-Masu

; TITLE OF INVENTION: Netrin Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 BUSH STREET, SUITE 3200

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA

; COUNTRY: USA

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; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030040046A1 Relevant
; TOPOLOGY: No. US20030040046A1 Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-933-261-5

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Query Match          97.0%; Score 419; DB 10; Length 898;
Best Local Similarity 96.3%; Pred. No. 1.5e-44;
Matches 79; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db      817 QKIIASLDPPCSRGA DWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLGQL 876

Qy      61 AAVAGLGQPDAGLFTVSEAE C 82
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Db      877 AAVAGLGQPDAGLFTVSEAE C 898

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RESULT 7

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US-09-970-944-13
; Sequence 13, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding
Same and
; TITLE OF INVENTION: Antibodies Directed Against these Proteins
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02

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; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-970-944-13
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```

; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030059859A1 Relevant
; TOPOLOGY: No. US20030059859A1 Relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-256-702-5

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Query Match          97.0%; Score 419; DB 14; Length 898;
Best Local Similarity 96.3%; Pred. No. 1.5e-44;
Matches 79; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 QKIISSLDPPCRRGADWRTLAAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
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Db      817 QKIIASLDPPCSR GADWRTLAAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLGQL 876

Qy      61 AAVAGLGQPDAGLFTVSEAEC 82
      |||||||||||||||||||
Db      877 AAVAGLGQPDAGLFTVSEAEC 898

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RESULT 9
US-10-240-154-16
; Sequence 16, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 898
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-240-154-16

```

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Query Match          97.0%; Score 419; DB 14; Length 898;
Best Local Similarity 96.3%; Pred. No. 1.5e-44;
Matches 79; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1 QKIISSLDPPCRRGADWRTLAAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
      ||||:||||| ||||||||||||||||||||||||||||||||||||||||| ||
Db      817 QKIIASLDPPCSR GADWRTLAAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLGQL 876

```

Qy 61 AAAVAGLGQPDAGLFTVSEAE 82
 |||||
 Db 877 AAAVAGLGQPDAGLFTVSEAE 898

RESULT 10

US-10-296-115-1104

; Sequence 1104, Application US/10296115

; Publication No. US20040053248A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq Inc

; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides

; FILE REFERENCE: 784PCT

; CURRENT APPLICATION NUMBER: US/10/296,115

; CURRENT FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: US09/488,725

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US09/552,317

; PRIOR FILING DATE: 2000-04-25

```
; NUMBER OF SEQ ID NOS: 1478
```

; SEQ ID NO 1104

; LENGTH: 436

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; TYPE: PRT
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; ORGANISM: Homo sapiens

US-10-296-115-1104

Query Match: 85.1%; Score 367.5; DB 15; Length 436;

Best Local Similarity 88.0%; Pred. No. 2.5e-38;

Matches 73; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

[illegible]

Db 354 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 413

Qy 61 AAVAGLGQPDAGLFT-VSEAEC 82
 | | | | | | | | : | | | |

Db 414 AAVAGTGPAGRWLLSQCSEAEC 436

RESULT 11

US-09-764-861-38

; Sequence 38, Application US/09764861

; Publication No. US20020086811A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PTZ04

; CURRENT APPLICATION NUMBER: US/09/764,861

; CURRENT FILING DATE: 2001-01-17

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; Prior application data removed - consult PALM or file wrapper
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; NUMBER OF SEQ ID NOS: 74
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; SOFTWARE: PatentIn Ver. 2.0
```

; SEQ ID NO 38

; LENGTH: 184

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; TYPE: PRT
```

; ORGANISM: Homo sapiens

; FEATURE:


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; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 476
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (163)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-476
```

```
Query Match          84.1%; Score 363.5; DB 14; Length 184;
Best Local Similarity 86.7%; Pred. No. 2.8e-38;
Matches 72; Conservative 1; Mismatches 9; Indels 1; Gaps 1;
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```
Qy      1 QKIISLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      102 QKIISLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 161

Qy      61 AAAVAGLGQPDAGLFT-VSEAEC 82
          | |||| | | : ||||
Db      162 AXAVAGTGPAGRWLLSQCSAEAC 184
```

RESULT 14

```
US-10-115-928-38
; Sequence 38, Application US/10115928
; Publication No. US20030092615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ04C1
; CURRENT APPLICATION NUMBER: US/10/115,928
; CURRENT FILING DATE: 2002-04-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (163)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-928-38
```

```
Query Match          84.1%; Score 363.5; DB 14; Length 184;
```


; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-933-261-6

Query Match 83.4%; Score 360.5; DB 10; Length 557;
Best Local Similarity 86.7%; Pred. No. 2.7e-37;
Matches 72; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

```
Qy      1 QKIISLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      475 QKIISLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 534

Qy      61 AAAVAGLGQPDAGLFT-VSEAEC 82
          |||||      | : |||||
Db      535 AAAVAGTXPAGRWLLSQCSEAEC 557
```

Search completed: March 1, 2005, 09:51:33
Job time : 16.7821 secs

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:46:18 ; Search time 3.20109 Seconds
(without alignments)
2464.715 Million cell updates/sec

Title: US-10-624-932-2_COPY_817_898
Perfect score: 432
Sequence: 1 QKIISLDPPCRRGADWRTL.....AVAGLGQPDAGLFTVSEAEC 82

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	138.5	32.1	919	2	T32541	unc-5 protein - Ca
2	138.5	32.1	947	1	B44294	unc-5 protein, lon
3	91.5	21.2	1125	2	T14892	transcription fact
4	87.5	20.3	1435	2	T32930	hypothetical prote
5	81	18.8	1423	1	I37275	death-associated p
6	75.5	17.5	907	2	I50404	p50B/p97 (Lyt-10)
7	73.5	17.0	522	2	I67414	nuclear factor kap
8	72.5	16.8	971	2	A35697	transcription fact
9	71.5	16.6	968	2	A37867	transcription fact
10	70.5	16.3	976	1	TVMSMD	macrophage colony-
11	69	16.0	900	2	A42024	transcription fact
12	69	16.0	933	2	S17233	transcription fact
13	68.5	15.9	858	2	S31761	potassium channel

14	67	15.5	219	2	D72739	hypothetical prote
15	66.5	15.4	984	2	A41996	NF-kappa-B p50 sub
16	64.5	14.9	433	2	AE2658	glycolate oxidase
17	64.5	14.9	433	2	B97440	glycolate oxidase
18	63.5	14.7	493	2	JC8027	type 1 angiotensin
19	63	14.6	253	2	AE3511	homospermidine syn
20	62.5	14.5	351	2	H70682	probable cysA - My
21	62	14.4	173	2	F71609	ribosomal protein
22	62	14.4	842	2	AB0674	probable hydrolase
23	61.5	14.2	189	2	D45188	chitin synthase (E
24	61.5	14.2	427	1	GQHUN	nerve growth facto
25	61.5	14.2	600	2	H84176	medium-chain acyl-
26	61	14.1	335	2	T34837	probable transfera
27	61	14.1	472	2	G83537	aromatic amino aci
28	60.5	14.0	1171	2	A42916	metabotropic gluta
29	60	13.9	225	2	T02660	germin-like protei
30	60	13.9	304	2	E70898	hypothetical prote
31	60	13.9	365	2	S31921	naringenin 3-dioxy
32	60	13.9	367	2	T31262	xylene monooxygena
33	60	13.9	367	2	S72924	hypothetical prote
34	60	13.9	370	2	G87212	conserved hypothet
35	60	13.9	514	2	T39458	DNA binding protei
36	60	13.9	1819	2	T26533	hypothetical prote
37	59.5	13.8	189	2	G45188	chitin synthase (E
38	59.5	13.8	415	2	B83634	hypothetical prote
39	59.5	13.8	978	2	S16385	macrophage colony-
40	59.5	13.8	1186	2	H88869	protein unc-31 [im
41	59.5	13.8	1270	2	T28087	hypothetical prote
42	59	13.7	370	2	F95927	probable mandelate
43	59	13.7	427	2	JN0785	Carbon catabolite
44	59	13.7	446	2	D70597	probable signal pe
45	59	13.7	469	2	G72602	hypothetical prote

ALIGNMENTS

RESULT 1

T32541

unc-5 protein - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T32541

R;Latreille, P.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of *C. elegans* cosmid B0273.

A;Reference number: Z21187

A;Accession: T32541

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-919 <LAT>

A;Cross-references: UNIPROT:O44171; EMBL:AF036698; PIDN:AAB88355.1;

GSPDB:GN00022; CESP:B0273.4a

A;Experimental source: strain Bristol N2; clone B0273

C;Genetics:

A;Gene: unc-5; CESP:B0273.4a

A;Map position: 4

A;Introns: 41/3; 108/1; 142/3; 201/1; 323/2; 553/1; 858/3
C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology;
thrombospondin type 1 repeat homology

Query Match 32.1%; Score 138.5; DB 2; Length 919;
Best Local Similarity 44.9%; Pred. No. 5.9e-08;
Matches 31; Conservative 12; Mismatches 23; Indels 3; Gaps 2;

Qy 7 LDPPCRRGADWRTLAQKLHLSHLSFFASKP--SPTAMILNLWEARHFPNGN-LSQLAAA 63
||| :||| ||:||| | :| |||| | ||::|:|||| : : |
Db 834 LDMPNESHSDWRGLAKKLHYDRYLQFFASFPDCSPTSLLLDLWEASSSGSARAVPDLLQT 893

Qy 64 VAGLGQPDA 72
: :|||
Db 894 LRVMGRPDA 902

RESULT 2

B44294

unc-5 protein, long form - *Caenorhabditis elegans*

N;Contains: unc-5 protein, short form

C;Species: *Caenorhabditis elegans*

C;Date: 30-Apr-1993 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004

C;Accession: B44294; T32540; A44294

R;Leung-Hagesteijn, C.; Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.;

Hedgecock, E.M.; Culotti, J.G.

Cell 71, 289-299, 1992

A;Title: UNC-5, a transmembrane protein with immunoglobulin and thrombospondin type 1 domains, guides cell and pioneer axon migrations in *C. elegans*.

A;Reference number: A44294; MUID:93046629; PMID:1384987

A;Contents: variety Bergerac

A;Accession: B44294

A;Molecule type: DNA

A;Residues: 1-947 <LEU>

A;Cross-references: UNIPROT:O44171; GB:S47168; NID:g258527; PIDN:AAB23867.1; PID:g258529

A;Note: sequence extracted from NCBI backbone (NCBIN:116668, NCBIN:116670, NCBIN:116672, NCBIN:116674, NCBIN:116676, NCBIN:116678, NCBIN:116680, NCBIN:116682, NCBIN:116685, NCBIP:118648)

A;Note: authors translated the codon CTA for residue 642 as Val; sequence shown follows the authors' translation

A;Note: mRNA lacking the first exon is equally prevalent

R;Latreille, P.

submitted to the EMBL Data Library, December 1997

A;Description: The sequence of *C. elegans* cosmid B0273.

A;Reference number: Z21187

A;Accession: T32540

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-947 <LAT>

A;Cross-references: EMBL:AF036698; PIDN:AAB88356.1; GSPDB:GN00022; CESP:B0273.4b

A;Experimental source: strain Bristol N2; clone B0273

C;Genetics:

A;Gene: unc-5

A;Map position: 4

A;Introns: 28/1; 69/3; 136/1; 170/3; 229/1; 351/2; 581/1; 886/3

C;Function:

A;Description: required for guidance of pioneering axons and cells migrating dorsally along the body wall; proposed to be a receptor on the surface of the motile cells
 C;Superfamily: unc-5 protein; immunoglobulin homology; SH3 homology; thrombospondin type 1 repeat homology
 C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane protein
 F;30-947/Product: unc-5 protein, short form #status predicted <ALT>
 F;46-116/Domain: immunoglobulin homology <IM1>
 F;153-211/Domain: immunoglobulin homology <IM2>
 F;229-300/Domain: thrombospondin type 1 repeat homology #status atypical <THR1>
 F;301-354/Domain: thrombospondin type 1 repeat homology <THR2>
 F;365-390/Domain: transmembrane #status predicted <TMM>
 F;512-559/Domain: SH3 homology <SH3>
 F;53-114,65-112,160-209/Disulfide bonds: #status predicted
 F;206/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 32.1%; Score 138.5; DB 1; Length 947;
 Best Local Similarity 44.9%; Pred. No. 6.2e-08;
 Matches 31; Conservative 12; Mismatches 23; Indels 3; Gaps 2;

Qy 7 LDPPCRRGADWRTLAQKLHLSHLSFFASKP--SPTAMILNLWEARHFPNGN-LSQLAAA 63
 ||| :||| ||:||| | :| |||| | ||:::|:|||| : : |
 Db 862 LDMPNESHSDWRGLAKKLHYDRYLQFFASFPDCSPTSLLLDLWEASSSGSARAVPDLLQT 921
 Qy 64 VAGLGQPD 72
 : :|:||||
 Db 922 LRVMGRPDA 930

RESULT 3

T14892

transcription factor NF-kappaB - sea urchin (*Strongylocentrotus purpuratus*)

C;Species: *Strongylocentrotus purpuratus* (purple urchin)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T14892

R;Pancer, Z.; Rast, J.P.; Davidson, E.H.

Immunogenetics 49, 773-786, 1999

A;Title: Origins of immunity: transcription factors and homologs of effector genes of the vertebrate immune system expressed in sea urchin coelomocytes.

A;Reference number: Z18253; MUID:99328904; PMID:10398804

A;Accession: T14892

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1125 <PAN>

A;Cross-references: UNIPROT:O96458; EMBL:AF064258; NID:g4165050; PID:g4165051; PIDN:AAD08653.1

C;Genetics:

A;Gene: NFkB

C;Superfamily: human transcription factor NF-kappa-B2; ankyrin repeat homology; rel homology

C;Keywords: DNA binding; nucleus; phosphoprotein; transcription regulation

Query Match 21.2%; Score 91.5; DB 2; Length 1125;
 Best Local Similarity 33.3%; Pred. No. 0.024;
 Matches 24; Conservative 14; Mismatches 31; Indels 3; Gaps 1;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 :|: | || | ||| :| | : |:| | ||||:| | :| | : :|
 Db 1012 EKLGSMLDDNYPTTQSWFTLANRLGLSNMLNFLKLVPSPTAVILKQFEAM---DGTIKEL 1068

Qy 61 AAAVAGLGQPD 72
 : : :|
 Db 1069 RDVLSSMNHIEA 1080

RESULT 4

T32930

hypothetical protein K12C11.4 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T32930

R;Wamsley, P.; Kramer, J.

submitted to the EMBL Data Library, January 1998

A;Description: The sequence of *C. elegans* cosmid K12C11.

A;Reference number: Z21248

A;Accession: T32930

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1435 <WAM>

A;Cross-references: UNIPROT:O44997; EMBL:AF043701; PIDN:AAB97579.1;

GSPDB:GN00019; CESP:K12C11.4

A;Experimental source: strain Bristol N2; clone K12C11

C;Genetics:

A;Gene: CESP:K12C11.4

A;Map position: 1

A;Introns: 79/2; 154/2; 267/2; 433/1; 533/3; 599/3; 691/3; 875/1; 1025/3;
 1169/3; 1348/3

C;Superfamily: death-associated protein kinase; ankyrin repeat homology; protein kinase homology

Query Match 20.3%; Score 87.5; DB 2; Length 1435;
 Best Local Similarity 34.8%; Pred. No. 0.092;
 Matches 24; Conservative 6; Mismatches 36; Indels 3; Gaps 1;

Qy 7 LDPPCRRGADWRTLAQKLHLD SHLSFFAS---KPSPTAMILNLWEARHFPNGNLSQLAAA 63
 |||| | || || || | : | | | :|| | | : :|
 Db 1323 LDPPHAMGRDWSILAVKLQLTDQVPDVDSTGQSLSRDQLLNEWAIHHPEQASVGNLCRI 1382

Qy 64 VAGLGQPD 72
 : ||: ||
 Db 1383 LVELGRCD 1391

RESULT 5

I37275

death-associated protein kinase (EC 2.7.1.-) - human

N;Alternate names: calmodulin-dependent protein kinase homolog; DAP kinase

C;Species: *Homo sapiens* (man)

C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 10-Jul-1998

C;Accession: I37275; S39269

R;Deiss, L.P.; Feinstein, E.; Berissi, H.; Cohen, O.; Kimchi, A.

Genes Dev. 9, 15-30, 1995

A;Title: Identification of a novel serine/threonine kinase and a novel 15-kD protein as potential mediators of the gamma interferon-induced cell death.
A;Reference number: A55614; MUID:95129831; PMID:7828849
A;Accession: I37275
A;Molecule type: mRNA
A;Residues: 1-1423 <RES>
A;Cross-references: EMBL:X76104; NID:g434846; PID:g434847
C;Genetics:
A;Gene: GDB:DAPK1; DAPK
A;Cross-references: GDB:555932; OMIM:600831
A;Map position: 9q34.1-9q34.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate using ATP
A;Pathway: apoptosis
A;Note: activity is calmodulin dependent
C;Superfamily: death-associated protein kinase; ankyrin repeat homology; protein kinase homology
C;Keywords: apoptosis; ATP; calmodulin binding; phosphotransferase; serine/threonine-specific protein kinase; tandem repeat
F;11-267/Domain: protein kinase homology <KIN>
F;19-27/Region: protein kinase ATP-binding motif
F;285-308/Region: calmodulin binding #status predicted
F;370-402/Domain: ankyrin repeat homology <AN1>
F;403-435/Domain: ankyrin repeat homology <AN2>
F;436-468/Domain: ankyrin repeat homology <AN3>
F;470-502/Domain: ankyrin repeat homology <AN4>
F;503-535/Domain: ankyrin repeat homology <AN5>
F;536-568/Domain: ankyrin repeat homology <AN6>
F;569-601/Domain: ankyrin repeat homology <AN7>
F;602-634/Domain: ankyrin repeat homology <AN8>
F;42,64,139,141/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 18.8%; Score 81; DB 1; Length 1423;
Best Local Similarity 28.8%; Pred. No. 0.52;
Matches 23; Conservative 12; Mismatches 35; Indels 10; Gaps 2;

```

Qy      1 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASK-----PSPTAMILNLWEARHF 52
          :|:  |||  | ||  ||  | |  :: : :  |||  :|  |  :
Db      1304 RKLSRLLDPPDPLGKDWCLLAMNLGLPDLVAKYNTNNGAPKDFLPSPLHALLREWTT--Y 1361

Qy      53 PNGNLSQLAAAVAGLGQPD 72
          |  :  | : :  ||: ||
Db      1362 PESTVGTLMSKLRRELGRDA 1381

```

RESULT 6
I50404

p50B/p97 (Lyt-10) transcription factor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50404
R;Ikeda, T.; Hirota, Y.; Onodera, T.
Gene 138, 193-196, 1994
A;Title: Isolation of a cDNA encoding the chicken p50B/p97 (Lyt-10) transcription factor.
A;Reference number: I50404; MUID:94171036; PMID:7510259

A;Accession: I50404
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-907 <IKE>
A;Cross-references: UNIPROT:P98150; GB:D16367; NID:g755083; PIDN:BAA03868.1;
PID:g755084
C;Genetics:
A;Gene: p50B
C;Superfamily: human transcription factor NF-kappa-B2; ankyrin repeat homology;
rel homology
F;37-341/Domain: rel homology <REL>

Query Match 17.5%; Score 75.5; DB 2; Length 907;
Best Local Similarity 32.7%; Pred. No. 1.4;
Matches 18; Conservative 11; Mismatches 23; Indels 3; Gaps 1;

Qy 14 GADWRTLQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLG 68
|::| |:::| | | : : |::: |: |: |::| | | :|
Db 795 GSDWMELAKRLGLCSLVETKYDTPSPSVLLRSYE---LAGGSLGGLLEALDSMG 846

RESULT 7

I67414
nuclear factor kappa B - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I67414
R;Hamil, K.G.; Hall, S.H.
Endocrinology 134, 1205-1212, 1994
A;Title: Cloning of rat Sertoli cell follicle-stimulating hormone primary
response complementary deoxyribonucleic acid: regulation of TSC-22 gene
expression.
A;Reference number: I53276; MUID:94164020; PMID:8161377
A;Accession: I67414
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-522 <RES>
A;Cross-references: UNIPROT:Q63369; GB:L26267; NID:g425471; PIDN:AAA20684.1;
PID:g474298
C;Superfamily: human transcription factor NF-kappa-B2; ankyrin repeat homology;
rel homology

Query Match 17.0%; Score 73.5; DB 2; Length 522;
Best Local Similarity 28.2%; Pred. No. 1.3;
Matches 20; Conservative 15; Mismatches 29; Indels 7; Gaps 2;

Qy 2 KIISSLDPPCRRGADWRTLQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLA 61
|::| | | :| | | | | | : | |::: |::: | | :|
Db 368 KLEIPDP---DKNWATLQKLGLGILNNAFRLSPAPSKTLMNDNYEV---SGGTIKELV 420
Qy 62 AAVAGLGQPD 72
|: |: |:|
Db 421 EALRQMGYTEA 431

RESULT 8

A35697

transcription factor NF-kappaB - mouse
N;Alternate names: nuclear factor kappa-B; p70
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 09-Jul-2004
C;Accession: A35697; A42144; I52824
R;Ghosh, S.; Gifford, A.M.; Riviere, L.R.; Tempst, P.; Nolan, G.P.; Baltimore, D.
Cell 62, 1019-1029, 1990
A;Title: Cloning of the p50 DNA binding subunit of NF-kappaB: homology to rel and dorsal.
A;Reference number: A35697; MUID:90367113; PMID:2203532
A;Accession: A35697
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-971 <GHO>
A;Cross-references: UNIPROT:P25799; GB:M57999; NID:g201931; PIDN:AAA40415.1; PID:g201932; GB:M37732
R;Inoue, J.; Kerr, L.D.; Kakizuka, A.; Verma, I.M.
Cell 68, 1109-1120, 1992
A;Title: I kappa B gamma, a 70 kd protein identical to the C-terminal half of p110 NF-kappa B: a new member of the I kappa B family.
A;Reference number: A42144; MUID:92191289; PMID:1339305
A;Accession: A42144
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 365-971 <INO>
A;Cross-references: GB:S89033; NID:g247616; PIDN:AAB21851.1; PID:g247617
A;Experimental source: RLM-11 T-cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:89033, NCBIP:89034)
R;Gerondakis, S.; Morrice, N.; Richardson, I.B.; Wettenhall, R.; Fecondo, J.; Grumont, R.J.
Cell Growth Differ. 4, 617-627, 1993
A;Title: The activity of a 70 kilodalton I kappa B molecule identical to the carboxyl terminus of the p105 NF-kappa B precursor is modulated by protein kinase A.
A;Reference number: I52824; MUID:94001687; PMID:8398903
A;Accession: I52824
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 365-971 <GER>
A;Cross-references: GB:S66656; NID:g436284; PIDN:AAB28573.1; PID:g436285
C;Superfamily: human transcription factor NF-kappa-B2; ankyrin repeat homology; rel homology
C;Keywords: DNA binding; nucleus; phosphoprotein; transcription regulation
F;40-364/Domain: rel homology <REL>
F;359-363/Region: nuclear location signal
F;335/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase)
#status predicted

Query Match 16.8%; Score 72.5; DB 2; Length 971;
Best Local Similarity 28.2%; Pred. No. 3.4;
Matches 20; Conservative 15; Mismatches 29; Indels 7; Gaps 2;

Qy 2 KIISSLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLA 61
|:: || :| ||||| | :| |:: :: :| |::|
Db 817 KLLIIPDP---DKNWATLAQKLGLGILNNAFRLSPAPSKTLMdNYEV---SGGTIKELM 869

Qy 62 AAVAGLGQPD 72
 |: :| :|
Db 870 EALQQMGYTEA 880

RESULT 9

A37867

transcription factor NF-kappa-B 50K chain precursor - human

N;Alternate names: nuclear factor of kappa light chain gene enhancer in B-cells (NF-kappa-B) DNA binding chain p105; transcription factor KBF1

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004

C;Accession: A37867; A35696; S13291; S58040; S58041; S58042; S58043; S58044; S58045; S58046; S58047; S58048; S58049; S58050; S58051; S58054; S58055; S58056; S58063; S58065; S58076; S58077

R;Meyer, R.; Hatada, E.N.; Hohmann, H.P.; Haiker, M.; Bartsch, C.; Roethlisberger, U.; Lahm, H.W.; Schlaeger, E.J.; van Loon, A.P.G.M.; Scheidereit, C.

Proc. Natl. Acad. Sci. U.S.A. 88, 966-970, 1991

A;Title: Cloning of the DNA-binding subunit of human nuclear factor kappaB: the level of its mRNA is strongly regulated by phorbol ester or tumor necrosis factor alpha.

A;Reference number: A37867; MUID:91126115; PMID:1992489

A;Accession: A37867

A;Molecule type: mRNA

A;Residues: 1-968 <MEY>

A;Cross-references: UNIPROT:P19838; GB:M58603; NID:g189177; PIDN:AAA36360.1; PID:g189178

R;Kieran, M.; Blank, V.; Logeat, F.; Vandekerckhove, J.; Lottspeich, F.; Le Bail, O.; Urban, M.B.; Kourilsky, P.; Baeuerle, P.A.; Israael, A.
Cell 62, 1007-1018, 1990

A;Title: The DNA binding subunit of NF-kappaB is identical to factor KBF1 and homologous to the rel oncogene product.

A;Reference number: A35696; MUID:90367112; PMID:2203531

A;Accession: A35696

A;Molecule type: mRNA

A;Residues: 1-39, 'A', 40-968 <KIE>

A;Cross-references: GB:M55643; GB:M37492; NID:g189179; PIDN:AAA36361.1; PID:g189180

R;Bours, V.; Villalobos, J.; Burd, P.R.; Kelly, K.; Siebenlist, U.
Nature 348, 76-80, 1990

A;Title: Cloning of a mitogen-inducible gene encoding a kappa-B DNA-binding protein with homology to the rel oncogene and to cell-cycle motifs.

A;Reference number: S13291; MUID:91043047; PMID:2234062

A;Accession: S13291

A;Molecule type: mRNA

A;Residues: 1-926, 'S', 928-968 <BOU>

R;Heron, E.; Deloukas, P.; van Loon, A.P.

submitted to the EMBL Data Library, January 1995

A;Description: The complete exon-intron structure of human NFKB1 encoding the p105 and p50 proteins of transcription factor NF-kappaB.

A;Reference number: S58040

A;Accession: S58040

A;Molecule type: DNA

A;Residues: 1-550, 'SS', 553-725, 'V', 727-868, 'I', 870-968 <HER>

A;Cross-references: EMBL:Z47734; EMBL:Z47735; EMBL:Z47736; EMBL:Z47737; EMBL:Z47738; EMBL:Z47739; EMBL:Z47740; EMBL:Z47741; EMBL:Z47742; EMBL:Z47743;

EMBL:Z47744; EMBL:Z47748; EMBL:Z47749; EMBL:Z47750; EMBL:Z47751; EMBL:Z47752;
 EMBL:Z47753; EMBL:Z47754; EMBL:Z47755
 C;Comment: This precursor is processed to a mature form designated p50 that binds DNA directly.
 C;Comment: NF-kappa-B exists primarily in an inactive cytoplasmic form that consists of a p50, p65, and an inhibitory chain I-kappa-B. Certain stimuli cause dissociation of the inhibitory chain and translocation to the nucleus.
 C;Genetics:
 A;Gene: GDB:NFKB1
 A;Cross-references: GDB:127544; OMIM:164011
 A;Map position: 4q24-4q24
 A;Introns: 13/3; 40/1; 52/3; 85/3; 135/2; 190/1; 243/1; 278/1; 308/3; 355/1; 403/1; 433/1; 498/1; 545/2; 583/3; 651/1; 707/3; 742/1; 783/3; 806/1; 863/3; 916/1
 C;Superfamily: human transcription factor NF-kappa-B2; ankyrin repeat homology; rel homology
 C;Keywords: DNA binding; duplication; nucleus; phosphoprotein; transcription regulation
 F;42-366/Domain: rel homology <REL>
 F;361-365/Region: nuclear location signal
 F;337/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase)
 #status predicted

Query Match 16.6%; Score 71.5; DB 2; Length 968;
 Best Local Similarity 28.2%; Pred. No. 4.4;
 Matches 20; Conservative 15; Mismatches 29; Indels 7; Gaps 2;

```
Qy      2 KIISSLDPPCRRGADWRTLQAKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLA 61
      |:: ||      :| ||||| |      : |      |::: :: :|      | : :|
Db      821 KLEIPDP----DKNWATLAQKLGLGILNNAFRLSPAPSKTLMDNYEV---SGGTVREL 873

Qy      62 AAVAGLGQPD 72
      |: :| :|
Db      874 EALRQMGYTEA 884
```

RESULT 10

TVMSMD

macrophage colony-stimulating factor 1 receptor precursor - mouse

N;Contains: protein-tyrosine kinase (EC 2.7.1.112) csflr/fms

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2000

C;Accession: S01880

R;Rothwell, V.M.; Rohrschneider, L.R.

Oncogene Res. 1, 311-324, 1987

A;Title: Murine c-fms cDNA: cloning, sequence analysis and retroviral expression.

A;Reference number: S01880; MUID:88217329; PMID:2966922

A;Accession: S01880

A;Molecule type: mRNA

A;Residues: 1-976 <ROT>

A;Cross-references: EMBL:X06368

C;Genetics:

A;Gene: fms

C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology; protein kinase homology

C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein; magnesium; phosphoprotein; phosphotransferase; proto-oncogene; receptor; transmembrane protein; tyrosine-specific protein kinase
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-976/Product: macrophage colony-stimulating factor 1 receptor #status predicted <MAT>
 F;20-515/Domain: extracellular #status predicted <EXT>
 F;35-86/Domain: immunoglobulin homology <IMM1>
 F;120-179/Domain: immunoglobulin homology <IMM2>
 F;217-280/Domain: immunoglobulin homology <IMM3>
 F;316-381/Domain: immunoglobulin homology <IMM4>
 F;410-485/Domain: immunoglobulin homology <IMM5>
 F;516-535/Domain: transmembrane #status predicted <TMM>
 F;536-976/Domain: intracellular #status predicted <INT>
 F;578-914/Domain: protein kinase homology <KIN>
 F;586-594/Region: protein kinase ATP-binding motif
 F;42-84,127-177,224-278,417-483/Disulfide bonds: #status predicted
 F;45,73,302,335,389,410,449,478,491/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;614,631,776/Active site: Lys, Glu, Asp #status predicted
 F;781,794/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 16.3%; Score 70.5; DB 1; Length 976;
 Best Local Similarity 32.2%; Pred. No. 5.8;
 Matches 29; Conservative 6; Mismatches 36; Indels 19; Gaps 4;

```

Qy      11 CRRGADWRTLQKLHL--DSHLSFFASKPSPTAMI-----LNLWEARHFPNGN 56
      || | || || | :| : || :| : : | ||
Db      432 CRGHTDRCDEAQLHLWNDRHPEVLSQKPFQKVI IQSQLPIGPKHNMITYFCKTHNSVGN 491

Qy      57 LSQLA AVAGLGQ----PDAGLFTVSEAE C 82
      || || : || | || || |
Db      492 SSQYFRAVS-LGQSKQLPDESLFTPVVVAC 520

```

RESULT 11

A42024

transcription factor NF-kappa-B2, p100 splice form - human

N;Alternate names: lyt-10; major histocompatibility complex class I-specific transcription factor NF-kappa-B2 100K chain; nuclear factor of kappa light chain gene enhancer in B-cells (NF-kappa-B) chain NFKB2; transcription factor H2TF1

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: A42024; A41645; A48525

R;Bours, V.; Burd, P.R.; Brown, K.; Villalobos, J.; Park, S.; Ryseck, R.P.; Bravo, R.; Kelly, K.; Siebenlist, U.

Mol. Cell. Biol. 12, 685-695, 1992

A;Title: A novel mitogen-inducible gene product related to p50/p105-NF-kappa B participates in transactivation through a kappa B site.

A;Reference number: A42024; MUID:92123193; PMID:1531086

A;Accession: A42024

A;Molecule type: mRNA

A;Residues: 1-900 <BOU>

A;Cross-references: UNIPROT:Q00653; GB:S76638; NID:g243420; PIDN:AAB21124.1; PID:g243421

A;Experimental source: peripheral blood T-cells

A;Note: sequence extracted from NCBI backbone (NCBIN:76638, NCBIP:76639)

R;Neri, A.; Chang, C.C.; Lombardi, L.; Salina, M.; Corradini, P.; Maiolo, A.T.; Chaganti, R.S.K.; Dalla-Favera, R.
 Cell 67, 1075-1087, 1991
 A;Title: B cell lymphoma-associated chromosomal translocation involves candidate oncogene *lyt-10*, homologous to NF-kappaB p50.
 A;Reference number: A41645; MUID:92103674; PMID:1760839
 A;Accession: A41645
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-42, 'A', 44-143, 'K', 145-432, 'EP', 435-454, 'HG', 457-469, 'A', 471-663, 'G', 665-748, 'RR', 751-754, 'DR', 757-763, 'R', 765-830, 'V', 832-859, 861-875, 'E', 877-900 <NER>
 R;Potter, D.A.; Larson, C.J.; Eckes, P.; Schmid, R.M.; Nabel, G.J.; Verdine, G.L.; Sharp, P.A.
 J. Biol. Chem. 268, 18882-18890, 1993
 A;Title: Purification of the major histocompatibility complex class I transcription factor H2TF1. The full-length product of the *nfkB2* gene.
 A;Reference number: A48525; MUID:93366804; PMID:8360178
 A;Accession: A48525
 A;Molecule type: protein
 A;Residues: 'K', 460-461, 'X', 463-469, 'A'; 'KX', 581-597; 'KX', 637-638, 'X', 640-645, 'X', 647 <POT>
 A;Experimental source: HeLa cells
 A;Note: sequence modified after extraction from NCBI backbone
 C;Comment: For other splice forms, see PIR:S17233, PIR:I38609, PIR:A57034.
 C;Comment: The full-length form of this protein is the MHC class I-specific transcription factor H2TF1. A processed form, designated NF-kappaB2 p52, may participate in a complex similar to NF-kappa-B.
 C;Genetics:
 A;Gene: GDB:NFKB2
 A;Cross-references: GDB:128804; OMIM:164012
 A;Map position: 10q24-10q24
 C;Superfamily: human transcription factor NF-kappa-B2; ankyrin repeat homology; rel homology
 C;Keywords: alternative splicing; DNA binding; nucleus; transcription factor; transcription regulation
 F;38-342/Domain: rel homology <REL>
 F;310-313/Region: nuclear location signal
 F;337-341/Region: nuclear location signal

Query Match 16.0%; Score 69; DB 2; Length 900;
 Best Local Similarity 29.4%; Pred. No. 8;
 Matches 20; Conservative 15; Mismatches 29; Indels 4; Gaps 2;

```

Qy      1 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
      | : || | :| : | ||::| | | : : ||: :| :| |::|
Db      776 QNLEQLLDGPEAQGS-WAELAERLGLRSLVDTYRQTTSPSGSLLRSYE---LAGGDLA 831

Qy      61 AAVAGLG 68
      |:::|
Db      832 LEALSDMG 839

```

RESULT 12
 S17233
 transcription factor NF-kappa-B2, p105 splice form - human

N;Alternate names: lyt-10; major histocompatibility complex class I-specific transcription factor NF-kappa-B2; nuclear factor of kappa light chain gene enhancer in B-cells (NF-kappa-B) chain 2 (NFKB2); transcription factor H2TF1 C;Species: Homo sapiens (man)
 C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
 C;Accession: S17233; A56343; I38064; S16736
 R;Schmid, R.M.; Perkins, N.D.; Duckett, C.S.; Andrews, P.C.; Nabel, G.J. Nature 352, 733-736, 1991
 A;Title: Cloning of an NF-kappa-B subunit which stimulates HIV transcription in synergy with p65.
 A;Reference number: S17233; MUID:91343004; PMID:1876189
 A;Accession: S17233
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-933 <SCH>
 A;Cross-references: UNIPROT:Q00653; EMBL:X61498; NID:g35039; PIDN:CAA43715.1; PID:g35040
 R;Liptay, S.; Schmid, R.M.; Nabel, E.G.; Nabel, G.J. Mol. Cell. Biol. 14, 7695-7703, 1994
 A;Title: Transcriptional regulation of NF-kappaB2: evidence for kappaB-mediated positive and negative autoregulation.
 A;Reference number: A56343; MUID:95059001; PMID:7969113
 A;Accession: A56343
 A;Molecule type: DNA
 A;Residues: 1-6 <LIP>
 R;Lombardi, L.; Ciana, P.; Cappellini, C.; Trecca, D.; Guerrini, L.; Migliazza, A.; Maiolo, A.T.; Neri, A. Nucleic Acids Res. 23, 2328-2336, 1995
 A;Title: Structural and functional characterization of the promoter regions of the NFKB2 gene.
 A;Reference number: I38064; MUID:95334390; PMID:7541912
 A;Accession: I38064
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-7 <LOM>
 A;Cross-references: EMBL:X83768; NID:g633221; PIDN:CAA58721.1; PID:g633222
 C;Comment: For other splice forms, see PIR:A42024, PIR:I38609, PIR:A57034.
 C;Genetics:
 A;Gene: GDB:NFKB2
 A;Cross-references: GDB:128804; OMIM:164012
 A;Map position: 10q24-10q24
 C;Superfamily: human transcription factor NF-kappa-B2; ankyrin repeat homology; rel homology
 C;Keywords: alternative splicing; DNA binding; nucleus; transcription factor; transcription regulation
 F;38-342/Domain: rel homology <REL>
 F;310-313/Region: nuclear location signal
 F;337-341/Region: nuclear location signal

Query Match 16.0%; Score 69; DB 2; Length 933;
 Best Local Similarity 29.4%; Pred. No. 8.3;
 Matches 20; Conservative 15; Mismatches 29; Indels 4; Gaps 2;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 | : ||| :||| ||::| | : : ||: :| :| |::|
 Db 775 QNLEQLLDGPEAQGS-WAELAERLGLRSLVDITYRQTTPSGSLLRSYE---LAGGDLA GL 830

Qy 61 AAVAGLG 68
 |:::|
Db 831 LEALSDMG 838

RESULT 13

S31761

potassium channel protein DRK1 - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S31761

R;Albrecht, B.; Lorra, C.; Stocker, K.; Pongs, O.

submitted to the EMBL Data Library, September 1992

A;Description: Cloning, expression and chromosomal localization of the delayed rectifier type K⁺ channel human 2.1 (h-DRK1) gene.

A;Reference number: S31761

A;Accession: S31761

A;Molecule type: DNA

A;Residues: 1-858 <ALB>

A;Cross-references: UNIPROT:Q14721; EMBL:X68302; NID:g30892; PIDN:CAA48374.1;

PID:g30893

C;Genetics:

A;Gene: GDB:KCNB1; KV2.1; DRK1

A;Cross-references: GDB:128081; OMIM:600397

A;Map position: 20q13.2-20q13.2

C;Superfamily: potassium channel protein drk1

Query Match 15.9%; Score 68.5; DB 2; Length 858;
Best Local Similarity 29.0%; Pred. No. 8.6;
Matches 18; Conservative 11; Mismatches 20; Indels 13; Gaps 2;

Qy 30 LSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLG-----QPDAGLFTVSE 79
 ::| ||| :| :: | | | ||||| |:: ::| :
Db 674 VNFMEGDPSPLLPVLGMY---HDPLRNRGSAAAVAGLECATLLDKAVLSPESSIYTTAS 730

Qy 80 AE 81
 |:
Db 731 AK 732

RESULT 14

D72739

hypothetical protein APE0446- Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: D72739

R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no,

K.; Takahashi, M.; Sekine, M.; Baba, S.; Ankai, A.; Kosugi, H.; Hosoyama, A.;

Fukui, S.; Nagai, Y.; Nishijima, K.; Nakazawa, H.; Takamiya, M.; Masuda, S.;

Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.;

Aoki, K.; Kubota, K.; Nakamura, Y.; Nomura, N.; Sako, Y.; Kikuchi, H.

DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix K1.

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: D72739

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-219 <KAW>
A;Cross-references: UNIPROT:Q9YHEY8; DDBJ:AP000059; NID:g5103911;
PIDN:BAA79408.1; PID:g5104092
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0446
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0284

Query Match 15.5%; Score 67; DB 2; Length 219;
Best Local Similarity 34.4%; Pred. No. 2.8;
Matches 22; Conservative 4; Mismatches 18; Indels 20; Gaps 3;

Qy 8 DPP---CRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAV 64
:|| ||||| | | | || | : ||: ||
Db 135 NPPFGVWRRGADWEVLEYALRL-----KPRAVYAIVK-----SGNMGFHAACA 177

Qy 65 AGLG 68
|||
Db 178 AGLG 181

RESULT 15

A41996
NF-kappa-B p50 subunit precursor p105 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C;Accession: A41996
R;Capobianco, A.J.; Chang, D.; Mosialos, G.; Gilmore, T.D.
J. Virol. 66, 3758-3767, 1992
A;Title: p105, the NF-kappa-B p50 precursor protein, is one of the cellular proteins complexed with the v-Rel oncoprotein in transformed chicken spleen cells.
A;Reference number: A41996; MUID:92260650; PMID:1533881
A;Accession: A41996
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-984 <CAP>
A;Cross-references: UNIPROT:Q04861; GB:M86930; NID:g212525; PIDN:AAA49000.1; PID:g212526
C;Superfamily: human transcription factor NF-kappa-B2; ankyrin repeat homology; rel homology
C;Keywords: DNA binding; nucleus; phosphoprotein; transcription regulation
F;47-371/Domain: rel homology <REL>
F;366-370/Region: nuclear location signal
F;342/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase)
#status predicted

Query Match 15.4%; Score 66.5; DB 2; Length 984;
Best Local Similarity 28.2%; Pred. No. 17;
Matches 20; Conservative 14; Mismatches 30; Indels 7; Gaps 2;

Qy 2 KIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLA 61
|::: || :| |||: || | : | |||: |: :: | :|
Db 820 KLETPDP----SKNWSTLAEKLGILNNAFQLSPSPSKTLLDNYK---ISGGTGQELI 872

Qy 62 AAVAGLGQPD 72

Db || : :|
 873 AAFTQMDHTEA 883

Search completed: March 1, 2005, 09:07:23
Job time : 4.20109 secs

OM protein - protein search, using sw model

Run on: March 1, 2005, 08:41:47 ; Search time 15.0005 Seconds
(without alignments)
2799.282 Million cell updates/sec

Title: US-10-624-932-2_COPY_817_898
Perfect score: 432
Sequence: 1 QKIISLDPPCRRGADWRTL.....AVAGLGQPDAGLFTVSEAE 82

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		8						
Result		Query						
No.	Score	Match	Length	DB	ID	Description		
1	432	100.0	842	1	UN5A_HUMAN	Q6zn44 homo sapien		
2	419	97.0	898	1	UN5A_MOUSE	Q8kls4 mus musculu		
3	419	97.0	898	1	UN5A_RAT	O08721 rattus norv		
4	221	51.2	931	1	UN5C_HUMAN	O95185 homo sapien		
5	221	51.2	931	1	UN5C_MOUSE	O08747 mus musculu		
6	221	51.2	931	1	UN5C_RAT	Q761x5 rattus norv		
7	217	50.2	931	1	UN5C_CHICK	Q7t2z5 gallus gall		
8	208	48.1	943	1	UN5B_XENLA	Q8jgt4 xenopus lae		
9	208	48.1	945	1	UN5B_MOUSE	Q8kls3 mus musculu		
10	205	47.5	945	1	UN5B_RAT	O08722 rattus norv		
11	199	46.1	945	1	UN5B_HUMAN	Q8izj1 homo sapien		
12	190	44.0	953	1	UN5D_HUMAN	Q6uxz4 homo sapien		
13	186	43.1	956	1	UN5D_MOUSE	Q8kls2 mus musculu		
14	161	37.3	325	2	Q8I1K1	Q8ilk1 drosophila		
15	159	36.8	876	2	Q7PW78	Q7pw78 anopheles g		

16	141	32.6	1072	1	UNC5_DROME	Q95tu8	drosophila
17	138.5	32.1	919	1	UNC5_CAEEL	Q26261	caenorhabdi
18	91.5	21.2	1125	2	O96458	O96458	strongyloce
19	87.5	20.3	1435	2	O44997	O44997	caenorhabdi
20	86	19.9	1427	2	Q6DDZ1	Q6ddz1	xenopus lae
21	83	19.2	1430	2	Q68CP8	Q68cp8	homo sapien
22	83	19.2	1442	1	DAK1_MOUSE	Q80ye7	mus musculu
23	82.5	19.1	518	2	Q8IV45	Q8iv45	homo sapien
24	82.5	19.1	958	1	KBF2_XENLA	O73630	xenopus lae
25	81	18.8	1432	1	DAK1_HUMAN	P53355	homo sapien
26	80	18.5	116	2	Q8C1L0	Q8c1l0	mus musculu
27	80	18.5	164	2	Q8BTQ8	Q8btq8	mus musculu
28	80	18.5	176	2	Q8K3C8	Q8k3c8	mus musculu
29	79.5	18.4	946	2	Q6DF61	Q6df61	xenopus tro
30	78	18.1	296	2	Q6Y1S1	Q6y1s1	rattus norv
31	77	17.8	1427	2	Q6NRK5	Q6nrk5	xenopus lae
32	76	17.6	906	1	KBF2_CHICK	P98150	gallus gall
33	74.5	17.2	933	2	Q68F05	Q68f05	xenopus lae
34	74.5	17.2	968	2	Q68D84	Q68d84	homo sapien
35	73.5	17.0	522	1	KBF1_RAT	Q63369	rattus norv
36	73.5	17.0	1005	2	O13075	O13075	gallus gall
37	73	16.9	216	2	Q9KXS8	Q9kxs8	streptomyce
38	73	16.9	518	2	Q6R653	Q6r653	mus musculu
39	72.5	16.8	971	1	KBF1_MOUSE	P25799	mus musculu
40	72.5	16.8	971	2	Q75ZL1	Q75zl1	mus musculu
41	71.5	16.6	550	2	Q8N4X7	Q8n4x7	homo sapien
42	71.5	16.6	654	2	Q6ZI88	Q6zi88	oryza sativ
43	71.5	16.6	968	1	KBF1_HUMAN	P19838	homo sapien
44	71.5	16.6	969	2	Q86V43	Q86v43	homo sapien
45	71	16.4	972	2	Q6F3J0	Q6f3j0	canis famil

ALIGNMENTS

RESULT 1

UN5A_HUMAN

ID UN5A_HUMAN STANDARD; PRT; 842 AA.
AC Q6ZN44; Q8TF26; Q96GP4;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
GN Name=UNC5A; Synonyms=KIAA1976, UNC5H1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,

RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 302-842 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 624-728 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=21842142; PubMed=11853319;
 RA Nagase T., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XXII.
 RT The complete sequences of 50 new cDNA clones which code for large

RT proteins.";
 RL DNA Res. 8:319-327(2001).
 RN [4]
 RP INDUCTION.
 RX PubMed=12598906; DOI=10.1038/ncb943;
 RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
 RT "p53RDL1 regulates of p53-dependent apoptosis.";
 RL Nat. Cell Biol. 5:216-223(2003).
 RN [5]
 RP DOWN-REGULATION IN CANCER.
 RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
 RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
 RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
 RT "The netrin-1 receptors UNC5H are putative tumor suppressors
 RT controlling cell death commitment.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with MAGED1. Interacts with PRKCABP, possibly mediating some
 CC interaction with PKC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
 CC with PRKCABP regulates its surface expression and leads to its
 CC removal from surface of neurons and growth cones (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q6ZN44-1; Sequence=Displayed;
 CC Note=No experimental confirmation available;
 CC Name=2;
 CC IsoId=Q6ZN44-2; Sequence=VSP_011694, VSP_011695;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q6ZN44-3; Sequence=VSP_011693;
 CC Note=No experimental confirmation available;
 CC -!- INDUCTION: By p53/TP53.
 CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
 CC participates in the induction of apoptosis (By similarity).
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues.
 CC Phosphorylated by PKC in vitro (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
 CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
 CC cancers.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 1 TSP type-1 domain.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.

CC -!- CAUTION: Ref.3 sequence differs from that shown due to the
CC presence of introns.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).

DR EMBL; AK131380; BAD18531.1; -.
DR EMBL; BC009333; AAH09333.2; -.
DR EMBL; BC033727; -; NOT_ANNOTATED_CDS.
DR EMBL; AB075856; BAB85562.1; ALT_SEQ.
DR Genew; HGNC:12567; UNC5A.
DR MIM; 607869; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 1.

KW Alternative splicing; Apoptosis; Developmental protein;
KW Immunoglobulin domain; Phosphorylation; Receptor; Signal;
KW Transmembrane.

FT	SIGNAL	1	25	Potential.
FT	CHAIN	26	842	Netrin receptor UNC5A.
FT	DOMAIN	1	306	Extracellular (Potential).
FT	TRANSMEM	307	327	Potential.
FT	DOMAIN	328	842	Cytoplasmic (Potential).
FT	DOMAIN	44	141	Ig-like.
FT	DOMAIN	155	234	Ig-like C2-type.
FT	DOMAIN	242	294	TSP type-1.
FT	DOMAIN	439	542	ZU5.
FT	DOMAIN	761	841	Death.
FT	SITE	340	341	Cleavage (by caspase-3) (By similarity).
FT	SITE	605	623	Interaction with DCC (By similarity).
FT	DISULFID	65	124	By similarity.
FT	DISULFID	170	221	By similarity.
FT	CARBOHYD	107	107	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	218	218	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	287	287	N-linked (GlcNAc. . .) (Potential).
FT	VARSPPLIC	1	97	MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPD
FT				LLPHFLVEPEDVYIVKNKPVLLVCKAVPATQIFFKCNGEWV
FT				RQVDHVIERSTDGSN -> MAGTSERSLISSISQPKAIECF
FT				EVKKKAFLTHGRYHGSGATPPKTKDPKPFETFCGQT (in
FT				isoform 3).
FT				/FTId=VSP_011693.
FT	VARSPPLIC	296	301	TASGPE -> SESSLP (in isoform 2).
FT				/FTId=VSP_011694.
FT	VARSPPLIC	302	842	Missing (in isoform 2).
FT				/FTId=VSP_011695.

SQ SEQUENCE 842 AA; 92958 MW; 3DFADCF973131849 CRC64;

Query Match 100.0%; Score 432; DB 1; Length 842;
Best Local Similarity 100.0%; Pred. No. 4.3e-41;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      761 QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 820

Qy      61 AAAVAGLGQPDAGLFTVSEAEC 82
        ||||||||||||||||||||
Db      821 AAAVAGLGQPDAGLFTVSEAEC 842
```

RESULT 2

UN5A_MOUSE

ID UN5A_MOUSE STANDARD; PRT; 898 AA.
AC Q8K1S4; Q6PEF7; Q80T71;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
GN Name=Unc5a; Synonyms=Kiaa1976, Unc5h1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
RA Engelkamp D.;
RT "Cloning of three mouse unc-5 genes and their expression patterns at
RT mid-gestation.";
RL Mech. Dev. 118:191-197(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:35-48(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand (By
CC similarity).

CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
CC with MAGED1. Interacts with PRKCABP, possibly mediating some
CC interaction with PKC (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
CC with PRKCABP regulates its surface expression and leads to its
CC removal from surface of neurons and growth cones (By similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC Name=1;

CC IsoId=Q8K1S4-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q8K1S4-2; Sequence=VSP_011697;

CC Note=No experimental confirmation available;

CC Name=3;

CC IsoId=Q8K1S4-3; Sequence=VSP_011696;

CC Note=No experimental confirmation available;

CC -!- TISSUE SPECIFICITY: Restricted to central nervous system.

CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
CC participates in the induction of apoptosis (By similarity).

CC -!- PTM: Phosphorylated by PKC in vitro. Phosphorylated on cytoplasmic
CC tyrosine residues (By similarity).

CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis (By similarity).

CC -!- SIMILARITY: Belongs to the UNC-5 family.

CC -!- SIMILARITY: Contains 1 death domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC -!- SIMILARITY: Contains 2 TSP type-1 domains.

CC -!- SIMILARITY: Contains 1 ZU5 domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----

DR EMBL; AJ487852; CAD32250.1; -.
 DR EMBL; AK122575; BAC65857.1; ALT_INIT.
 DR EMBL; BC058084; AAH58084.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:894682; Unc5a.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 898 Netrin receptor UNC5A.
 FT DOMAIN 26 361 Extracellular (Potential).
 FT TRANSMEM 362 382 Potential.
 FT DOMAIN 383 898 Cytoplasmic (Potential).
 FT DOMAIN 44 141 Ig-like.
 FT DOMAIN 155 234 Ig-like C2-type.
 FT DOMAIN 242 296 TSP type-1 1.
 FT DOMAIN 298 350 TSP type-1 2.
 FT DOMAIN 495 598 ZU5.
 FT DOMAIN 817 897 Death.
 FT SITE 396 397 Cleavage (by caspase-3) (By similarity).
 FT SITE 661 679 Interaction with DCC (By similarity).
 FT DISULFID 65 124 By similarity.
 FT DISULFID 170 221 By similarity.
 FT CARBOHYD 107 107 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 218 218 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 343 343 N-linked (GlcNAc . . .) (Potential).
 FT VARSPLIC 1 790 Missing (in isoform 3).
 FT /FTId=VSP_011696.
 FT VARSPLIC 241 296 Missing (in isoform 2).
 FT /FTId=VSP_011697.
 FT CONFLICT 217 217 A -> P (in Ref. 3).
 SQ SEQUENCE 898 AA; 98856 MW; 59F04BA2E196C1DB CRC64;

Query Match 97.0%; Score 419; DB 1; Length 898;
 Best Local Similarity 96.3%; Pred. No. 1.5e-39;

Matches 79; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 QKIISLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
      |||:||||| ||||||||||||||||||||||||||||||||||||||||| ||
Db      817 QKIITSLDPPCSR GADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLGQL 876

Qy      61 AA AVAGLGQPDAGLFTVSEAEC 82
      ||||||||||||||||
Db      877 AA AVAGLGQPDAGLFTVSEAEC 898
```

RESULT 3

UN5A_RAT

ID UN5A_RAT STANDARD; PRT; 898 AA.
AC O08721;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5A precursor (Unc-5 homolog A) (Unc-5 homolog 1).
GN Name=Unc5a; Synonyms=Unc5h1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Ventral spinal cord;
RX MEDLINE=97271897; PubMed=9126742;
RA Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,
RA Tessier-Lavigne M.;
RT "Vertebrate homologues of C. elegans UNC-5 are candidate netrin
RT receptors.";
RL Nature 386:833-838(1997).
RN [2]
RP FUNCTION, AND INTERACTION WITH DCC.
RX PubMed=10399920;
RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
RA Stein E.;
RT "A ligand-gated association between cytoplasmic domains of UNC5 and
RT DCC family receptors converts netrin-induced growth cone attraction to
RT repulsion.";
RL Cell 97:927-941(1999).
RN [3]
RP TISSUE SPECIFICITY.
RX PubMed=11472849;
RA Barrett C., Guthrie S.;
RT "Expression patterns of the netrin receptor UNC5H1 among developing
RT motor neurons in the embryonic rat hindbrain.";
RL Mech. Dev. 106:163-166(2001).
RN [4]
RP FUNCTION.
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
RL EMBO J. 20:2715-2722(2001).
RN [5]

RP FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION WITH MAGED1.
 RX PubMed=12598531; DOI=10.1074/jbc.M300415200;
 RA Williams M.E., Strickland P., Watanabe K., Hinck L.;
 RT "UNC5H1 induces apoptosis via its juxtamembrane region through an
 RT interaction with NRAGE.";
 RL J. Biol. Chem. 278:17483-17490 (2003).
 RN [6]
 RP INTERACTION WITH PRKCABP, PHOSPHORYLATION, AND MUTAGENESIS OF
 RP 896-ALA--CYS-898.
 RX PubMed=14672991; DOI=23/36/11279;
 RA Williams M.E., Wu S.C.-Y., McKenna W.L., Hinck L.;
 RT "Surface expression of the netrin receptor UNC5H1 is regulated through
 RT a protein kinase C-interacting protein/protein kinase-dependent
 RT mechanism.";
 RL J. Neurosci. 23:11279-11288 (2003).

CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with MAGED1. Interacts with PRKCABP, possibly mediating some
 CC interaction with PKC.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. The interaction
 CC with PRKCABP regulates its surface expression and leads to its
 CC removal from surface of neurons and growth cones.
 CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
 CC neurons. Expressed at early stages of neural tube development in
 CC the ventral spinal cord. In developing hindbrain, it colocalizes
 CC with a number of cranial motor neuron subpopulations from
 CC embryonic E11 to E14, while DCC is expressed by motor neurons at
 CC E12. Also expressed in non-neural structures, such as the basal
 CC plane of the hindbrain and midbrain, in the developing
 CC hypothalamus, thalamus and in the pallidum.
 CC -!- DOMAIN: The ZU5 domain mediates the interaction with MAGED1, which
 CC participates in the induction of apoptosis.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity). Phosphorylated by PKC in vitro.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.

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CC -----
DR EMBL; U87305; AAB57678.1; -.
DR HSSP; P07996; 1LSL.
DR RGD; 621755; Unc5h1.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Apoptosis; Developmental protein; Immunoglobulin domain;
KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 898 Netrin receptor UNC5A.
FT DOMAIN 26 361 Extracellular (Potential).
FT TRANSMEM 362 382 Potential.
FT DOMAIN 383 898 Cytoplasmic (Potential).
FT DOMAIN 44 141 Ig-like.
FT DOMAIN 155 238 Ig-like C2-type.
FT DOMAIN 242 296 TSP type-1 1.
FT DOMAIN 298 350 TSP type-1 2.
FT DOMAIN 495 598 ZU5.
FT DOMAIN 817 897 Death.
FT SITE 396 397 Cleavage (by caspase-3) (By similarity).
FT SITE 661 679 Interaction with DCC (By similarity).
FT DISULFID 65 124 By similarity.
FT DISULFID 170 221 By similarity.
FT CARBOHYD 107 107 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 218 218 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 343 343 N-linked (GlcNAc . . .) (Potential).
FT MUTAGEN 896 898 Missing: Abolishes interaction with
FT PRKCABP.
SQ SEQUENCE 898 AA; 98840 MW; 7A3CBCB9E7ACA135 CRC64;

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Query Match 97.0%; Score 419; DB 1; Length 898;
Best Local Similarity 96.3%; Pred. No. 1.5e-39;
Matches 79; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 QKIISSLDPPCRRGADWRTLAQKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
   ||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 817 QKIIASLDPPCSRGADWRTLAQKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLGQL 876

Qy 61 AAVAGLGQPDAGLFTVSEAE 82
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

```

RESULT 4

UN5C_HUMAN

ID UN5C_HUMAN STANDARD; PRT; 931 AA.
AC O95185; Q8IUT0;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3).
GN Name=UNC5C; Synonyms=UNC5H3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=99000841; PubMed=9782087; DOI=10.1006/geno.1998.5425;
RA Ackerman S.L., Knowles B.B.;
RT "Cloning and mapping of the UNC5C gene to human chromosome 4q21-q23.";
RL Genomics 52:205-208(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP DOWN-REGULATION IN CANCER.
RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
RT "The netrin-1 receptors UNC5H are putative tumor suppressors
RT controlling cell death commitment.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous

CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. Also involved in corticospinal tract axon guidances
 CC independently of DCC. It also acts as a dependence receptor
 CC required for apoptosis induction when not associated with netrin
 CC ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O95185-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O95185-2; Sequence=VSP_011700, VSP_011701;
 CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in
 CC kidney. Not expressed in developing or adult lung.
 CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
 CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
 CC phosphatase, suggesting that its activity is regulated by
 CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
 CC netrin-dependent (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
 CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
 CC cancers.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.

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DR EMBL; AF055634; AAC67491.1; -.
 DR EMBL; BC041156; AAH41156.1; -.
 DR HSSP; P07996; 1LSL.
 DR Genew; HGNC:12569; UNC5C.
 DR MIM; 603610; -.
 DR GO; GO:0005042; F:netrin receptor activity; TAS.
 DR GO; GO:0007411; P:axon guidance; TAS.
 DR GO; GO:0007420; P:brain development; TAS.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.

DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 40 Potential.
 FT CHAIN 41 931 Netrin receptor UNC5C.
 FT DOMAIN 41 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 931 Cytoplasmic (Potential).
 FT DOMAIN 62 159 Ig-like.
 FT DOMAIN 161 256 Ig-like C2-type.
 FT DOMAIN 260 314 TSP type-1 1.
 FT DOMAIN 316 368 TSP type-1 2.
 FT DOMAIN 528 631 ZU5.
 FT DOMAIN 850 929 Death.
 FT SITE 415 416 Cleavage (by caspase-3) (By similarity).
 FT SITE 694 712 Interaction with DCC (By similarity).
 FT DISULFID 83 142 By similarity.
 FT DISULFID 188 239 By similarity.
 FT MOD_RES 568 568 Phosphotyrosine (By similarity).
 FT CARBOHYD 236 236 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc . . .) (Potential).
 FT VARSPLIC 370 370 T -> SFIYPISTEQRTQNEYGFSS (in isoform 2).
 FT /FTId=VSP_011700.
 FT VARSPLIC 579 931 Missing (in isoform 2).
 FT /FTId=VSP_011701.
 FT VARIANT 37 37 G -> V (in dbSNP:2306715).
 FT /FTId=VAR_019731.
 FT VARIANT 721 721 T -> M (in dbSNP:2289043).
 FT /FTId=VAR_019732.
 FT CONFLICT 219 219 T -> I (in Ref. 1).
 FT CONFLICT 489 489 S -> T (in Ref. 1).
 SQ SEQUENCE 931 AA; 103101 MW; EFD71122C98DABB8 CRC64;

Query Match 51.2%; Score 221; DB 1; Length 931;
 Best Local Similarity 51.9%; Pred. No. 1.3e-16;
 Matches 42; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 ||: |||| | || ||| || ||: || :||: ||: || || :||: ||||: ||: |||| |
 Db 850 QKLCSSLDAPQTRGHDWRMLAHKLNLDRLNYFATKSSPTGVILDLWEAQNFDPGNLSML 909
 Qy 61 AAAGVAGLGQPDAGLFTVSEAE 81
 || : ||: : : : || :

RESULT 5

UN5C_MOUSE

ID UN5C_MOUSE STANDARD; PRT; 931 AA.
AC O08747; Q8CD16;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)
DE (Rostral cerebellar malformation protein).
GN Name=Unc5c; Synonyms=Rcm, Unc5h3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, DISEASE, AND TISSUE
RP SPECIFICITY.
RC STRAIN=C57B6/SJL;
RX MEDLINE=97271898; PubMed=9126743;
RA Ackerman S.L., Kozak L.P., Przyborski S.A., Rund L.A., Boyer B.B.,
RA Knowles B.B.;
RT "The mouse rostral cerebellar malformation gene encodes an UNC-5-like
RT protein.";
RL Nature 386:838-842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP FUNCTION, AND TISSUE SPECIFICITY.
 RX PubMed=9389662;
 RA Przyborski S.A., Knowles B.B., Ackerman S.L.;
 RT "Embryonic phenotype of Unc5h3 mutant mice suggests chemorepulsion
 RT during the formation of the rostral cerebellar boundary.";
 RL Development 125:41-50(1998).
 RN [4]
 RP INTERACTION WITH DCC.
 RX PubMed=10399920;
 RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
 RA Stein E.;
 RT "A ligand-gated association between cytoplasmic domains of UNC5 and
 RT DCC family receptors converts netrin-induced growth cone attraction to
 RT repulsion.";
 RL Cell 97:927-941(1999).
 RN [5]
 RP PHOSPHORYLATION SITE TYR-568, AND MUTAGENESIS OF TYR-568.
 RX PubMed=11533026; DOI=10.1074/jbc.M103872200;
 RA Tong J., Killeen M., Steven R., Binns K.L., Culotti J., Pawson T.;
 RT "Netrin stimulates tyrosine phosphorylation of the UNC-5 family of
 RT netrin receptors and induces Shp2 binding to the RCM cytodomain.";
 RL J. Biol. Chem. 276:40917-40925(2001).
 RN [6]
 RP FUNCTION.
 RX PubMed=12451134; DOI=22/23/10346;
 RA Finger J.H., Bronson R.T., Harris B., Johnson K., Przyborski S.A.,
 RA Ackerman S.L.;
 RT "The netrin 1 receptors Unc5h3 and Dcc are necessary at multiple
 RT choice points for the guidance of corticospinal tract axons.";
 RL J. Neurosci. 22:10346-10356(2002).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. Also involved in corticospinal tract axon guidances
 CC independently of DCC. It also acts as a dependence receptor
 CC required for apoptosis induction when not associated with netrin
 CC ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=008747-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=008747-2; Sequence=VSP_011702;
 CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
 CC neurons. Highly expressed in brain and lung. Weakly expressed in
 CC testis, ovary, spleen, thymus and bladder. Expressed at very low
 CC level in kidney, intestine and salivary gland.
 CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
 CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
 CC phosphatase, suggesting that its activity is regulated by

CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
 CC netrin-dependent.
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- DISEASE: Defects in Unc5c are the cause of rostral cerebellar
 CC malformation (Rcm). Rcm is characterized by cerebellar and
 CC midbrain defects, apparently as a result of abnormal neuronal
 CC migration.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
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 CC -----
 DR EMBL; U72634; AAB54103.1; -.
 DR EMBL; AK031655; BAC27495.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:1095412; Unc5c.
 DR GO; GO:0005886; C:plasma membrane; IC.
 DR GO; GO:0005042; F:netrin receptor activity; IDA.
 DR GO; GO:0005515; F:protein binding; IDA.
 DR GO; GO:0007420; P:brain development; IMP.
 DR GO; GO:0030334; P:regulation of cell migration; IMP.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 40 Potential.

FT	CHAIN	41	931	Netrin receptor UNC5C.
FT	DOMAIN	41	380	Extracellular (Potential).
FT	TRANSMEM	381	401	Potential.
FT	DOMAIN	402	931	Cytoplasmic (Potential).
FT	DOMAIN	62	159	Ig-like.
FT	DOMAIN	161	256	Ig-like C2-type.
FT	DOMAIN	260	314	TSP type-1 1.
FT	DOMAIN	316	368	TSP type-1 2.
FT	DOMAIN	528	631	ZU5.
FT	DOMAIN	850	929	Death.
FT	SITE	415	416	Cleavage (by caspase-3) (By similarity).
FT	SITE	694	712	Interaction with DCC (By similarity).
FT	DISULFID	83	142	By similarity.
FT	DISULFID	188	239	By similarity.
FT	MOD_RES	568	568	Phosphotyrosine.
FT	CARBOHYD	236	236	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	361	361	N-linked (GlcNAc. . .) (Potential).
FT	VARSPPLIC	370	370	A -> GFIIYPISTEHRPQNEYGFSS (in isoform 2).
FT				/FTId=VSP_011702.
FT	MUTAGEN	568	568	Y->F: Abolishes interaction with PTPN11,
FT				leading to a increased level of
FT				phosphorylation.
FT	CONFLICT	16	16	L -> I (in Ref. 2).
FT	CONFLICT	733	733	H -> R (in Ref. 2).
FT	CONFLICT	924	924	S -> Y (in Ref. 2).
SQ	SEQUENCE	931 AA;	103062 MW;	8A5D951A4EECA179 CRC64;

Query Match 51.2%; Score 221; DB 1; Length 931;
 Best Local Similarity 51.9%; Pred. No. 1.3e-16;
 Matches 42; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

Qy	1	QKIISSLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL	60
		: : : : : : : : :	
Db	850	QKLCSSLDAPQTRGHDWRMLAHKLNLDRLNYFATKSSPTGVILDLWEAQNFDPGNLSML	909
Qy	61	AAAVAGLGQPDAGLFTVSEAE	81
		: : : : : :	
Db	910	AAVLEEMGRHETVVSLLAAEGQ	930

RESULT 6

UN5C_RAT

ID UN5C_RAT STANDARD; PRT; 931 AA.
 AC Q761X5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3).
 GN Name=Unc5c; Synonyms=Unc5h3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND DISEASE.
 RX PubMed=15010202; DOI=10.1016/j.molbrainres.2003.12.003;
 RA Kuramoto T., Kuwamura M., Serikawa T.;

RT "Rat neurological mutations cerebellar vermis defect and hobble are
RT caused by mutations in the netrin-1 receptor gene Unc5h3.";
RL Brain Res. Mol. Brain Res. 122:103-108(2004).
RN [2]
RP FUNCTION.
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
RL EMBO J. 20:2715-2722(2001).

CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. Also involved in corticospinal tract axon guidances
CC independently of DCC. It also acts as a dependence receptor
CC required for apoptosis induction when not associated with netrin
CC ligand.
CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: Mainly expressed in brain. Also expressed in
CC kidney. Not expressed in developing or adult lung.
CC -!- PTM: Phosphorylated on different cytoplasmic tyrosine residues.
CC Phosphorylation of Tyr-568 leads to an interaction with PTPN11
CC phosphatase, suggesting that its activity is regulated by
CC phosphorylation/dephosphorylation. Tyrosine phosphorylation is
CC netrin-dependent (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis.
CC -!- DISEASE: Defects in Unc5c are the cause of cerebellar vermis
CC defect (cvd) and hobble (hob) phenotypes. Cvd and hob rats exhibit
CC cerebellar and midbrain defects, possibly as a result of abnormal
CC neuronal migration, and exhibit laminar structure abnormalities in
CC the fused cerebellar hemispheres and ectopic cerebellar tissues in
CC the cerebello-pontine junction.
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.

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CC -----

DR EMBL; AB118026; BAD05181.1; -.
DR RGD; 735109; Unc5c.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 40 Potential.
 FT CHAIN 41 931 Netrin receptor UNC5C.
 FT DOMAIN 41 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 931 Cytoplasmic (Potential).
 FT DOMAIN 62 159 Ig-like.
 FT DOMAIN 161 256 Ig-like C2-type.
 FT DOMAIN 260 314 TSP type-1 1.
 FT DOMAIN 316 368 TSP type-1 2.
 FT DOMAIN 528 631 ZU5.
 FT DOMAIN 850 929 Death.
 FT SITE 415 416 Cleavage (by caspase-3) (By similarity).
 FT SITE 694 712 Interaction with DCC (By similarity).
 FT DISULFID 83 142 By similarity.
 FT DISULFID 188 239 By similarity.
 FT MOD_RES 568 568 Phosphotyrosine (By similarity).
 FT CARBOHYD 236 236 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc . .) (Potential).
 SQ SEQUENCE 931 AA; 103134 MW; 25B183A97BCB8401 CRC64;

Query Match 51.2%; Score 221; DB 1; Length 931;
 Best Local Similarity 51.9%; Pred. No. 1.3e-16;
 Matches 42; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 ||: |||| | || ||| || ||: || :||: ||: || ||| :||: ||||: ||: |||| |
 Db 850 QKLCSSLDAPQTRGHDWRMLAHKLNLDRLNYFATKSSPTGVILDLWEAQNFDPGNLSML 909
 Qy 61 AAVAGLGQPDAGLFTVSEAE 81
 || : ||: : : : | :
 Db 910 AAVLEEMGRHETTVVSLAEGQ 930

RESULT 7
 UN5C_CHICK
 ID UN5C_CHICK STANDARD; PRT; 931 AA.
 AC Q7T2Z5;

DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5C precursor (Unc-5 homolog C) (Unc-5 homolog 3)
 DE (cUNC-5H3).
 GN Name=UNC5C;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX PubMed=12799087;
 RA Guan W., Condic M.L.;
 RT "Characterization of Netrin-1, Neogenin and cUNC-5H3 expression during
 RT chick dorsal root ganglia development.";
 RL Gene Expr. Patterns 3:369-373(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Restricted to proprioceptive neurons.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
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 CC -----
 DR EMBL; AY187310; AA067275.1; -.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.

KW Developmental protein; Immunoglobulin domain; Phosphorylation;
 KW Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 39 Potential.
 FT CHAIN 40 931 Netrin receptor UNC5C.
 FT DOMAIN 40 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 931 Cytoplasmic (Potential).
 FT DOMAIN 62 159 Ig-like.
 FT DOMAIN 161 256 Ig-like C2-type.
 FT DOMAIN 260 314 TSP type-1 1.
 FT DOMAIN 316 368 TSP type-1 2.
 FT DOMAIN 528 631 ZU5.
 FT DOMAIN 850 929 Death.
 FT DISULFID 83 142 By similarity.
 FT DISULFID 188 239 By similarity.
 FT CARBOHYD 236 236 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 361 361 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 931 AA; 102906 MW; 1E23A0D84F2E2C62 CRC64;

Query Match 50.2%; Score 217; DB 1; Length 931;
 Best Local Similarity 53.2%; Pred. No. 3.8e-16;
 Matches 42; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 ||: |||| | || ||| || || | :||: ||: | || | :||: ||||: ||: |||| |
 Db 850 QKLCSSLDAPQTRGHDWRMLAHKLKLD RYLN YFATKSSPTGVILD LWEAQNFDPGNLSML 909
 Qy 61 AA AVAGLGQPDAGLFTVSE 79
 || : ||: : : : |
 Db 910 AAVLEEMGRHETVVSLAAE 928

RESULT 8

UN5B_XENLA

ID UN5B_XENLA STANDARD; PRT; 943 AA.
 AC Q8JGT4;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (UNC-5 homolog) (Protein XUNC-5).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=22239703; PubMed=12351179; DOI=10.1016/S0925-4773(02)00215-0;
 RA Anderson R.B., Holt C.E.;
 RT "Expression of UNC-5 in the developing Xenopus visual system."
 RL Mech. Dev. 118:157-160(2002).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: In the developing visual system, it is
 CC expressed within the developing optic vesicles and later become

CC restricted to the dorsal ciliary marginal zone, a site of
 CC retinoblast proliferation and differentiation.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AY099459; AAM34486.1; -.
 DR HSSP; P07996; 1LSL.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Developmental protein; Immunoglobulin domain; Phosphorylation;
 KW Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 30 Potential.
 FT CHAIN 31 943 Netrin receptor UNC5B.
 FT DOMAIN 31 380 Extracellular (Potential).
 FT TRANSMEM 381 401 Potential.
 FT DOMAIN 402 943 Cytoplasmic (Potential).
 FT DOMAIN 51 148 Ig-like.
 FT DOMAIN 150 245 Ig-like C2-type.
 FT DOMAIN 249 303 TSP type-1 1.
 FT DOMAIN 305 357 TSP type-1 2.
 FT DOMAIN 540 643 ZU5.
 FT DOMAIN 863 941 Death.
 FT DISULFID 72 131 By similarity.
 FT DISULFID 177 228 By similarity.
 FT CARBOHYD 225 225 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 350 350 N-linked (GlcNAc . .) (Potential).

SQ SEQUENCE 943 AA; 105083 MW; A024E24A7EDB6175 CRC64;

Query Match 48.1%; Score 208; DB 1; Length 943;
Best Local Similarity 48.8%; Pred. No. 4.3e-15;
Matches 40; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
||| :||| | || ||| ||||| :| :|::||:| ||| :||:|||| | :|:|: |
Db 862 QKICNSLDAPNSRGNDWRLLAQKLCMDRYLNYFATKASPTGVILDLWEALHQDDGDLNTL 921

Qy 61 AAAVAGLGQPDAGLFTVSEAE 82
|:: :|: : | :: :|
Db 922 ASALEEMGKSEMMLVMATDGDC 943

RESULT 9

UN5B_MOUSE

ID UN5B_MOUSE STANDARD; PRT; 945 AA.
AC Q8K1S3; Q6PFH0; Q80Y85; Q9D398;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).
GN Name=Unc5b; Synonyms=Unc5h2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
RA Engelkamp D.;
RT "Cloning of three mouse unc-5 genes and their expression patterns at
RT mid-gestation.";
RL Mech. Dev. 118:191-197(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP TISSUE SPECIFICITY.
 RX PubMed=12799072;
 RA Dalvin S., Anselmo M.A., Prodhon P., Komatsuzaki K., Schnitzer J.J.,
 RA Kinane T.B.;
 RT "Expression of Netrin-1 and its two receptors DCC and UNC5H2 in the
 RT developing mouse lung.";
 RL Gene Expr. Patterns 3:279-283(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand (By
 CC similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC. Interacts
 CC with GNAI2 via its cytoplasmic part (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8K1S3-1; Sequence=Displayed;

```

CC      Name=2;
CC      IsoId=Q8K1S3-2; Sequence=VSP_011699;
CC      -!- TISSUE SPECIFICITY: Highly expressed in brain. Expressed in lung
CC          during late development. Expressed during early blood vessel
CC          formation, in the semicircular canal and in a dorsal to ventral
CC          gradient in the retina.
CC      -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC          similarity).
CC      -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC          cleavage does not take place when the receptor is associated with
CC          netrin ligand. Its cleavage by caspases is required to induce
CC          apoptosis (By similarity).
CC      -!- SIMILARITY: Belongs to the UNC-5 family.
CC      -!- SIMILARITY: Contains 1 death domain.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC      -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC      -!- SIMILARITY: Contains 1 ZU5 domain.
CC      -----
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CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AJ487853; CAD32251.1; -.
DR      EMBL; AK018177; BAB31108.1; -.
DR      EMBL; BC048162; AAH48162.1; ALT_INIT.
DR      EMBL; BC057560; AAH57560.1; -.
DR      HSSP; P07996; 1LSL.
DR      MGD; MGI:894703; Unc5b.
DR      InterPro; IPR000488; Death.
DR      InterPro; IPR011029; DEATH_like.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003598; Ig_c2.
DR      InterPro; IPR000884; TSP1.
DR      InterPro; IPR008085; TSP_1.
DR      InterPro; IPR000906; ZU5.
DR      Pfam; PF00531; Death; 1.
DR      Pfam; PF00047; ig; 1.
DR      Pfam; PF00090; TSP_1; 2.
DR      Pfam; PF00791; ZU5; 1.
DR      PRINTS; PR01705; TSP1REPEAT.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00408; IGc2; 1.
DR      SMART; SM00209; TSP1; 2.
DR      SMART; SM00218; ZU5; 1.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
DR      PROSITE; PS50092; TSP1; 2.
KW      Alternative splicing; Apoptosis; Developmental protein;
KW      Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
KW      Transmembrane.
FT      SIGNAL          1      26      Potential.
FT      CHAIN           27      945      Netrin receptor UNC5B.

```

FT	DOMAIN	27	377	Extracellular (Potential).
FT	TRANSMEM	378	398	Potential.
FT	DOMAIN	399	945	Cytoplasmic (Potential).
FT	DOMAIN	48	145	Ig-like.
FT	DOMAIN	153	242	Ig-like C2-type.
FT	DOMAIN	246	300	TSP type-1 1.
FT	DOMAIN	302	354	TSP type-1 2.
FT	DOMAIN	541	644	ZU5.
FT	DOMAIN	865	943	Death.
FT	SITE	412	413	Cleavage (by caspase-3) (By similarity).
FT	SITE	707	725	Interaction with DCC (By similarity).
FT	DISULFID	69	128	By similarity.
FT	DISULFID	174	225	By similarity.
FT	CARBOHYD	222	222	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	347	347	N-linked (GlcNAc. . .) (Potential).
FT	VARSPLIC	356	367	NQRTLNDPKSHP -> T (in isoform 2).
FT				/FTId=VSP_011699.
FT	CONFLICT	238	238	T -> A (in Ref. 2).
FT	CONFLICT	394	394	V -> E (in Ref. 2).
FT	CONFLICT	679	679	T -> S (in Ref. 2).
FT	CONFLICT	874	874	N -> D (in Ref. 2).
SQ	SEQUENCE	945 AA;	103738 MW;	80E896F0F0E06012 CRC64;

Query Match 48.1%; Score 208; DB 1; Length 945;
 Best Local Similarity 48.8%; Pred. No. 4.3e-15;
 Matches 40; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

Qy	1	QKIISSLDPPCRRGADWRTLAQKLHLSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL	60
		: : :: : : : : ::	
Db	864	QKICSSLDAPNSRGNDWRLLAQKLSMDRYLNYFATKASPTGVILDLWEARQQDDGDLNSL	923
Qy	61	AAAVAGLGQPDAGLFTVSEAE	82
		:: : : : : : :: :	
Db	924	ASALEEMGKSEMLVAMATDGDC	945

RESULT 10

UN5B_RAT

ID	UN5B_RAT	STANDARD;	PRT;	945 AA.
AC	O08722;			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2).			
GN	Name=Unc5b; Synonyms=Unc5h2;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE			
RP	SPECIFICITY.			
RX	MEDLINE=97271897; PubMed=9126742;			
RA	Leonardo E.D., Hinck L., Masu M., Keino-Masu K., Ackerman S.L.,			
RA	Tessier-Lavigne M.;			
RT	"Vertebrate homologues of C. elegans UNC-5 are candidate netrin			
RT	receptors.";			

RL Nature 386:833-838(1997).
RN [2]
RP FUNCTION, AND INTERACTION WITH DCC.
RX PubMed=10399920;
RA Hong K., Hinck L., Nishiyama M., Poo M.-M., Tessier-Lavigne M.,
RA Stein E.;
RT "A ligand-gated association between cytoplasmic domains of UNC5 and
RT DCC family receptors converts netrin-induced growth cone attraction to
RT repulsion.";
RL Cell 97:927-941(1999).

RN [3]
RP FUNCTION, AND MUTAGENESIS OF ASP-412.
RX PubMed=11387206; DOI=10.1093/emboj/20.11.2715;
RA Llambi F., Causeret F., Bloch-Gallego E., Mehlen P.;
RT "Netrin-1 acts as a survival factor via its receptors UNC5H and DCC.";
RL EMBO J. 20:2715-2722(2001).

CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
CC axon repulsion of neuronal growth cones in the developing nervous
CC system upon ligand binding. Axon repulsion in growth cones may be
CC caused by its association with DCC that may trigger signaling for
CC repulsion. It also acts as a dependence receptor required for
CC apoptosis induction when not associated with netrin ligand.
CC -!- SUBUNIT: Interacts with GNAI2 via its cytoplasmic part (By
CC similarity). Interacts with the cytoplasmic part of DCC.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Mainly expressed in regions of differentiating
CC neurons. Expressed in the developing sensory ganglia that flank
CC the spinal cord from E12, peaking at E14. Expressed in the roof
CC plate region of the spinal cord from E14.
CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
CC similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleavage does not take place when the receptor is associated with
CC netrin ligand. Its cleavage by caspases is required to induce
CC apoptosis.
CC -!- SIMILARITY: Belongs to the UNC-5 family.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.

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CC -----

DR EMBL; U87306; AAB57679.1; -.
DR HSSP; P07996; 1LSL.
DR RGD; 621756; Unc5h2.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.

DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR SMART; SM00218; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 945 Netrin receptor UNC5B.
 FT DOMAIN 27 377 Extracellular (Potential).
 FT TRANSMEM 378 398 Potential.
 FT DOMAIN 399 945 Cytoplasmic (Potential).
 FT DOMAIN 48 145 Ig-like.
 FT DOMAIN 153 242 Ig-like C2-type.
 FT DOMAIN 246 300 TSP type-1 1.
 FT DOMAIN 302 354 TSP type-1 2.
 FT DOMAIN 541 644 ZU5.
 FT DOMAIN 865 943 Death.
 FT SITE 412 413 Cleavage (by caspase-3).
 FT SITE 707 725 Interaction with DCC.
 FT DISULFID 69 128 By similarity.
 FT DISULFID 174 225 By similarity.
 FT CARBOHYD 222 222 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 347 347 N-linked (GlcNAc . . .) (Potential).
 FT MUTAGEN 412 412 D->N: Abolishes cleavage by caspase-3 and
 subsequent induction of apoptosis.
 SQ SEQUENCE 945 AA; 103520 MW; 6E9C2A262E560B9B CRC64;

Query Match 47.5%; Score 205; DB 1; Length 945;
 Best Local Similarity 47.6%; Pred. No. 9.5e-15;
 Matches 39; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRGRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 ||| :||| | || ||| ||||| :| :||:|:| ||| :||:||||| :||:| |
 Db 864 QKICNSLDAPNSRGNDWRLLAQKLSDRYLNyFATKASPTGVILDLEWARQQDDGDLNSL 923
 Qy 61 AAVAGLGQPDAGLFTVSEAE 82
 |:|: |:|: : : : : : : :
 Db 924 ASALEEMGKSEMLVAMTTDGDC 945

RESULT 11

UN5B_HUMAN

ID UN5B_HUMAN STANDARD; PRT; 945 AA.
 AC Q8IZJ1; Q86SN3; Q8N1Y2; Q9H9F3;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5B precursor (Unc-5 homolog B) (Unc-5 homolog 2)
 DE (p53-regulated receptor for death and life protein 1)
 DE (UNQ1883/PRO4326).
 GN Name=UNC5B; Synonyms=P53RDL1, UNC5H2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION
 RP WITH GNAI2.
 RC TISSUE=Lung;
 RX MEDLINE=22246081; PubMed=12359238; DOI=10.1016/S0006-291X(02)02277-5;
 RA Komatsuzaki K., Dalvin S., Kinane T.B.;
 RT "Modulation of G(ialpha(2)) signaling by the axonal guidance molecule
 RT UNC5H2.";
 RL Biochem. Biophys. Res. Commun. 297:898-905(2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, AND MUTAGENESIS OF ASP-412.
 RX PubMed=12598906; DOI=10.1038/ncb943;
 RA Tanikawa C., Matsuda K., Fukuda S., Nakamura Y., Arakawa H.;
 RT "p53RDL1 regulates of p53-dependent apoptosis.";
 RL Nat. Cell Biol. 5:216-223(2003).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [4]
 RP SEQUENCE OF 361-945 FROM N.A.
 RC TISSUE=Amygdala, and Teratocarcinoma;
 RX PubMed=14702039; DOI=10.1038/ngl285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,

RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [5]
 RP DOWN-REGULATION IN CANCER.
 RX PubMed=12655055; DOI=10.1073/pnas.0738063100;
 RA Thiebault K., Mazelin L., Pays L., Llambi F., Joly M.-O.,
 RA Scoazec J.-Y., Saurin J.-C., Romeo G., Mehlen P.;
 RT "The netrin-1 receptors UNC5H are putative tumor suppressors
 RT controlling cell death commitment.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4173-4178(2003).
 CC -!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
 CC axon repulsion of neuronal growth cones in the developing nervous
 CC system upon ligand binding. Axon repulsion in growth cones may be
 CC caused by its association with DCC that may trigger signaling for
 CC repulsion. It also acts as a dependence receptor required for
 CC apoptosis induction when not associated with netrin ligand.
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity). Interacts with GNAI2 via its cytoplasmic part.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8IZJ1-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8IZJ1-2; Sequence=VSP_011698;
 CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Also expressed at
 CC lower level in developing lung, cartilage, kidney and
 CC hematopoietic and immune tissues.
 CC -!- INDUCTION: By p53/TP53.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis.
 CC -!- MISCELLANEOUS: Down-regulated in multiple cancers including
 CC colorectal, breast, ovary, uterus, stomach, lung, or kidney
 CC cancers.
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
CC -!- SIMILARITY: Contains 1 ZU5 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY126437; AAM95701.1; -.
DR EMBL; AB096256; BAC57998.1; -.
DR EMBL; AY358351; AAQ88717.1; -.
DR EMBL; AK022859; BAB14276.1; ALT_INIT.
DR EMBL; AK094595; BAC04382.1; ALT_INIT.
DR HSSP; P07996; 1LSL.
DR Genew; HGNC:12568; UNC5B.
DR MIM; 607870; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP_1.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00090; TSP_1; 2.
DR Pfam; PF00791; ZU5; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00209; TSP1; 2.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50092; TSP1; 2.
KW Alternative splicing; Apoptosis; Developmental protein;
KW Immunoglobulin domain; Phosphorylation; Polymorphism; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 945 Netrin receptor UNC5B.
FT DOMAIN 27 377 Extracellular (Potential).
FT TRANSMEM 378 398 Potential.
FT DOMAIN 399 945 Cytoplasmic (Potential).
FT DOMAIN 48 145 Ig-like.
FT DOMAIN 147 242 Ig-like C2-type.
FT DOMAIN 246 300 TSP type-1 1.
FT DOMAIN 302 354 TSP type-1 2.
FT DOMAIN 541 644 ZU5.
FT DOMAIN 865 943 Death.
FT SITE 412 413 Cleavage (by caspase-3).
FT SITE 707 725 Interaction with DCC (By similarity).
FT DISULFID 69 128 By similarity.
FT DISULFID 174 225 By similarity.

FT CARBOHYD 222 222 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 347 347 N-linked (GlcNAc. . .) (Potential).
 FT VARSPLIC 356 367 NKKTLSDPNSHL -> M (in isoform 2).
 FT /FTId=VSP_011698.
 FT VARIANT 516 516 A -> T (in dbSNP:10509332).
 FT /FTId=VAR_019730.
 FT MUTAGEN 412 412 D->N: Abolishes cleavage by caspase-3 and
 FT subsequent induction of apoptosis.
 FT CONFLICT 483 483 K -> E (in Ref. 3).
 FT CONFLICT 851 851 L -> P (in Ref. 3; BAB14276).
 SQ SEQUENCE 945 AA; 103637 MW; 56064E335F323447 CRC64;

Query Match 46.1%; Score 199; DB 1; Length 945;
 Best Local Similarity 46.3%; Pred. No. 4.7e-14;
 Matches 38; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRRGADWRTLAQKLHLDSHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 ||| :||| | || ||| ||||| :| :||:|:| | ||| :||:| ||| :|:| :|
 Db 864 QKICNSLDAPNSRGNDWRMLAQKLSMDRYLNYFATKASPTGVILDLWEALQQDDGDLNSL 923

Qy 61 AAVAGLGQPDAGLFTVSEAEC 82
 |:|: |:|: : : : : : :|
 Db 924 ASALEEMGKSEMLVAVATDGDC 945

RESULT 12

UN5D_HUMAN

ID UN5D_HUMAN STANDARD; PRT; 953 AA.
 AC Q6UXZ4; Q8WYP7;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4)
 DE (UNQ6012/PRO34692).
 GN Name=UNC5D; Synonyms=KIAA1777, UNC5H4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;
 RA Nakajima D., Nakayama M., Nagase T., Ohara O.;
 RT "Identification of unc5H4 gene.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Receptor for netrin. May be involved in axon guidance by
 CC mediating axon repulsion of neuronal growth cones in the
 CC developing nervous system upon ligand binding. Axon repulsion in
 CC growth cones may be caused by its association with DCC that may
 CC trigger signaling for repulsion. It also acts as a dependence
 CC receptor required for apoptosis induction when not associated with
 CC netrin ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q6UXZ4-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q6UXZ4-2; Sequence=VSP_011703;
 CC Note=No experimental confirmation available;
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB055056; BAB83663.1; -.
 DR EMBL; AY358147; AAQ88514.1; -.
 DR HSSP; P07996; 1LSL.
 DR Genew; HGNC:18634; UNC5D.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.

DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Alternative splicing; Apoptosis; Developmental protein;
 KW Immunoglobulin domain; Phosphorylation; Receptor; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 953 Netrin receptor UNC5D.
 FT DOMAIN 33 379 Extracellular (Potential).
 FT TRANSMEM 380 400 Potential.
 FT DOMAIN 401 953 Cytoplasmic (Potential).
 FT DOMAIN 54 151 Ig-like.
 FT DOMAIN 153 244 Ig-like C2-type.
 FT DOMAIN 252 306 TSP type-1 1.
 FT DOMAIN 308 360 TSP type-1 2.
 FT DOMAIN 540 642 ZU5.
 FT DOMAIN 859 936 Death.
 FT SITE 416 417 Cleavage (by caspase-3) (By similarity).
 FT SITE 703 721 Interaction with DCC (By similarity).
 FT DISULFID 75 134 By similarity.
 FT DISULFID 180 231 By similarity.
 FT CARBOHYD 117 117 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 228 228 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 353 353 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 376 376 N-linked (GlcNAc . . .) (Potential).
 FT VARSPLIC 1 34 MGRAAATAGGGGGARRWLPWLGLCFWAAGTAAAR -> MIL
 FT VLVKALSDVCAGTSGFLLDFSSQTSP (in isoform
 FT 2).
 FT /FTId=VSP_011703.
 SQ SEQUENCE 953 AA; 105879 MW; 5F893B9DF746F731 CRC64;

Query Match 44.0%; Score 190; DB 1; Length 953;
 Best Local Similarity 44.4%; Pred. No. 5.2e-13;
 Matches 36; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 |:| :: | | :| ||: |||| :: :||:|:: ||:|:||||||| :|:| |
 Db 859 QRICATFDTPNAGKGDWQMLAQKNSINRNLSYFATQSSPSAVILNLWEARHQHDGDLDSL 918
 Qy 61 AAVAGLGQPDAGLFTVSEAE 81
 | |: :: | :||:
 Db 919 ACALEEIGRTHTKLSNISESQ 939

RESULT 13

UN5D_MOUSE

ID UN5D_MOUSE STANDARD; PRT; 956 AA.
 AC Q8K1S2;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Netrin receptor UNC5D precursor (Unc-5 homolog D) (Unc-5 homolog 4).
 GN Name=Unc5d; Synonyms=Unc5h4;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=22239710; PubMed=12351186; DOI=10.1016/S0925-4773(02)00248-4;
 RA Engelkamp D.;
 RT "Cloning of three mouse Unc5 genes and their expression patterns at
 RT mid-gestation.";
 RL Mech. Dev. 118:191-197(2002).
 CC -!- FUNCTION: Receptor for netrin involved in cell migration. May be
 CC involved in axon guidance by mediating axon repulsion of neuronal
 CC growth cones in the developing nervous system upon ligand binding.
 CC Axon repulsion in growth cones may be caused by its association
 CC with DCC that may trigger signaling for repulsion. It also acts as
 CC a dependence receptor required for apoptosis induction when not
 CC associated with netrin ligand (By similarity).
 CC -!- SUBUNIT: Interacts with the cytoplasmic part of DCC (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in developing limb and mammary
 CC gland.
 CC -!- PTM: Phosphorylated on cytoplasmic tyrosine residues (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
 CC cleavage does not take place when the receptor is associated with
 CC netrin ligand. Its cleavage by caspases is required to induce
 CC apoptosis (By similarity).
 CC -!- SIMILARITY: Belongs to the UNC-5 family.
 CC -!- SIMILARITY: Contains 1 death domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -!- SIMILARITY: Contains 2 TSP type-1 domains.
 CC -!- SIMILARITY: Contains 1 ZU5 domain.
 CC -----
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 CC -----
 DR EMBL; AJ487854; CAD32252.1; -.
 DR HSSP; P07996; 1LSL.
 DR MGD; MGI:2389364; Unc5d.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008085; TSP_1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF00090; TSP_1; 2.

DR Pfam; PF00791; ZU5; 1.
 DR PRINTS; PR01705; TSP1REPEAT.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00209; TSP1; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 KW Apoptosis; Developmental protein; Immunoglobulin domain;
 KW Phosphorylation; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 30 Potential.
 FT CHAIN 31 956 Netrin receptor UNC5D.
 FT DOMAIN 31 382 Extracellular (Potential).
 FT TRANSMEM 383 403 Potential.
 FT DOMAIN 404 956 Cytoplasmic (Potential).
 FT DOMAIN 52 149 Ig-like.
 FT DOMAIN 151 242 Ig-like C2-type.
 FT DOMAIN 250 304 TSP type-1 1.
 FT DOMAIN 306 358 TSP type-1 2.
 FT DOMAIN 543 645 ZU5.
 FT DOMAIN 862 939 Death.
 FT SITE 419 420 Cleavage (by caspase-3) (By similarity).
 FT SITE 706 724 Interaction with DCC (By similarity).
 FT DISULFID 73 132 By similarity.
 FT DISULFID 178 229 By similarity.
 FT CARBOHYD 115 115 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 226 226 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 351 351 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 379 379 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 956 AA; 106351 MW; DEDF07839C10C68D CRC64;

Query Match 43.1%; Score 186; DB 1; Length 956;
 Best Local Similarity 43.2%; Pred. No. 1.5e-12;
 Matches 35; Conservative 21; Mismatches 25; Indels 0; Gaps 0;

Qy 1 QKIISSLDPPCRRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 |:| ::| | :| ||: ||| :: :||:|::| ||:| ||||| ||:| |
 Db 862 QRICATFDTNPNAKGKDWQMLAQKNSINRNLSYFATQSSPSAVILNLWEARHQDGDLDLDSL 921
 Qy 61 AAVAGLGQPDAGLFTVSEAE 81
 | |: |:| :| ::| :
 Db 922 ACALEEIGRTHTKLSNITEPQ 942

RESULT 14

Q8I1K1

ID Q8I1K1 PRELIMINARY; PRT; 325 AA.
 AC Q8I1K1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Unc-5 (Fragment).
 GN Name=unc-5;
 OS Drosophila virilis (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.

DR EMBL; AAAB01008984; EAA14755.1; -.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR000906; ZU5.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00090; TSP_1; 2.
 DR Pfam; PF00791; ZU5; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS50092; TSP1; 2.
 FT NON_TER 1 1
 FT NON_TER 876 876
 SQ SEQUENCE 876 AA; 96301 MW; 6F9336D53E096E00 CRC64;

Query Match 36.8%; Score 159; DB 2; Length 876;
 Best Local Similarity 43.1%; Pred. No. 1.9e-09;
 Matches 31; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

Qy 1 QKIISLDPPCRGRGADWRTLAQKLHLD SHLSFFASKPSPTAMILNLWEARHFPNGNLSQL 60
 :|: |||| :: ||| || |::| :|::|::|::| ||: || |:
 Db 801 RKLRCCLDPPTQKRNDWRMLAAHLNVDRYLT YFATRPSP TDQILDLEWCNRNRLNALQQL 860
 Qy 61 AA AVAGLGQPD A 72
 : :|||
 Db 861 IEICRTMERPD A 872

Search completed: March 1, 2005, 09:03:42
 Job time : 16.0005 secs